

OM protein - protein search, using sw model  
 Run on: July 27, 2006, 11:54:57 ; Search time 198 Seconds  
 (without alignments)  
 1380.886 Million cell updates/sec

Title: US-10-677-669-69  
 Perfect score: 3135  
 Sequence: 1 MCSRVPLLLPLLLALPGP.....PLMGFGPGGLQSPHLHAKPYI 598  
 Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5  
 Total number of hits satisfying chosen parameters: 2589679  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
 Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1500 summaries

Database : A Geneseq 8:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description
RESULT 1					
ID	AA06484	standard; protein; 598 AA.			
DE	Human tumour-associated protein PRO357.				
PN	WO9935170-A2.				
PD	15-JUL-1999.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 3135;	DB 2;	Length 598;	
Best Local Similarity	100.0%;	Pred. No. 4e-190;			
RESULT 2					
ID	AA01322	standard; protein; 598 AA.			
DE	Human PRO357 polypeptide.				
PN	WO200032776-A2.				
PD	08-JUN-2000.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 3135;	DB 3;	Length 598;	
Best Local Similarity	100.0%;	Pred. No. 4e-190;			
RESULT 3					
ID	AA93691	standard; protein; 598 AA.			
DE	Amino acid sequence of novel polypeptide PRO357.				
PN	WO200037640-A2.				
PD	29-JUN-2000.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 3135;	DB 3;	Length 598;	
Best Local Similarity	100.0%;	Pred. No. 4e-190;			
RESULT 4					
ID	AA083643	standard; protein; 598 AA.			
DE	Human PRO protein, Seq ID No 104.				
PN	WO200208288-A2.				
PD	31-JAN-2002.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 3135;	DB 5;	Length 598;	
Best Local Similarity	100.0%;	Pred. No. 4e-190;			
RESULT 5					
ID	ADY31844	standard; protein; 598 AA.			
DE	Novel human secreted and transmembrane protein PRO357.				
PN	WO200193983-A1.				
PD	13-DEC-2001.				
PA	(GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 3135;	DB 5;	Length 598;	
Best Local Similarity	100.0%;	Pred. No. 4e-190;			
RESULT 6					
ID	ABU55931	standard; protein; 598 AA.			
DE	Human secreted/transmembrane protein PRO357.				

PN US2002142959-A1.  
 PD 03-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;  
 RESULT 7  
 ID ABU0790 standard; protein; 598 AA.  
 DE Human PRO polypeptide #52.  
 PN US2003036635-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;  
 RESULT 8  
 ID ABO33756 standard; protein; 598 AA.  
 DE Novel human secreted and transmembrane protein PRO357.  
 PN US2003045687-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;  
 RESULT 9  
 ID ABU60241 standard; protein; 598 AA.  
 DE Human PRO polypeptide #12.  
 PN US2002132768-A1.  
 PD 19-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;  
 RESULT 10  
 ID ABU64927 standard; protein; 598 AA.  
 DE Human secreted/transmembrane protein PRO357.  
 PN US2002173463-A1.  
 PD 21-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;  
 RESULT 11  
 ID ABU58361 standard; protein; 598 AA.  
 DE Novel human secreted protein PRO357.  
 PN US2002150976-A1.  
 PD 17-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;  
 RESULT 12  
 ID ABU57247 standard; protein; 598 AA.  
 DE Human PRO357 protein.  
 PN US2002142958-A1.  
 PD 03-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;  
 RESULT 13  
 ID ABU56312 standard; protein; 598 AA.  
 DE Human secreted/transmembrane protein, PRO357.  
 PN US2002132981-A1.  
 PD 19-SEP-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;  
 RESULT 14  
 ID ABU60352 standard; protein; 598 AA.  
 DE Novel human secreted and transmembrane protein PRO357.  
 PN US2002168715-A1.  
 PD 14-NOV-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 100.0%; Score 3135; DB 6; Length 598;  
 RESULT 15  
 ID ABU82099 standard; protein; 598 AA.  
 DE Novel human secreted and transmembrane protein PRO357.  
 PN US2003088063-A1.



PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 16  
ID ABU11313 standard; protein; 598 AA.  
DE Human pro357 protein sequence.  
PN US2002127643-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 17  
ID ABU671132 standard; protein; 598 AA.  
DE Human PRO polypeptide #12.  
PN US2002165143-A1.  
PD 07-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 18  
ID ABU72279 standard; protein; 598 AA.  
DE Human PRO357 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 19  
ID ABU72407 standard; protein; 598 AA.  
DE Human PRO357 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 20  
ID ABO34302 standard; protein; 598 AA.  
DE Human secreted/transmembrane polypeptide PRO 357.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 6; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 21  
ID ABU72109 standard; protein; 598 AA.  
DE Human membrane bound receptor/protein PRO357 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 22  
ID ADB83594 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 23  
ID ADB80700 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 24  
ID ADB73241 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096968-A1.  
PD 22-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 25  
ID ADB78323 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 26  
ID ADB84971 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 27  
ID ADB78077 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 28  
ID ADB87143 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 29  
ID ADB84725 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 30  
ID ADB83840 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 31  
ID ADB72995 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 32  
ID ADC25825 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2002142419-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 7; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 33  
ID ADC25583 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2002156004-A1.  
PD 24-OCT-2002.  
PA (GETH ) GENENTECH INC.



Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 34  
ID ADC25704 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003077698-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 35  
ID ADC36833 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 36  
ID ADC21823 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 37  
ID ADC49854 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 38  
ID ADC49053 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 39  
ID ADC49570 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 40  
ID ADC47431 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 41  
ID ADC47176 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 42  
ID ADC78051 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;

Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 43  
ID ADD06286 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 44  
ID ADC77805 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 45  
ID ADD50768 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 46  
ID ADD51014 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 47  
ID ADD50495 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 48  
ID ADD50249 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 49  
ID ADD51260 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 50  
ID ADH27489 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003083479-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 7; Length 598;  
RESULT 51  
ID ADC48807 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003092888-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;



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RESULT 52
ID ADE20978 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 53
ID ADE05822 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 54
ID ADD75051 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 55
ID ADD75797 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 56
ID ADD85029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 57
ID ADD86855 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 58
ID ADE20732 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 59
ID ADE39029 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 60
ID ADE05576 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 61
ID ADD85535 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 62
ID ADD78401 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 63
ID ADE21224 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 64
ID ADD77339 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 65
ID ADE20486 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 66
ID ADD75551 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 67
ID ADD74067 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 68
ID ADD74313 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 69
ID ADD76043 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3135; DB 8; Length 598;
Best Local Similarity 100.0%; Pred. No. 4e-190;
RESULT 70
ID ADD85535 standard; protein; 598 AA.
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DE Novel human secreted and transmembrane protein PRO357.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 71
ID ADE05084 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 72
ID ADD75297 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 73
ID ADD76841 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 74
ID ADD86609 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 75
ID ADD78077 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 76
ID ADE71538 standard; protein; 598 AA.
DE Human secreted/transmembrane PRO polypeptide #12.
PN US2003096742-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 77
ID ADD77585 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 78
ID ADD77831 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 79
ID ADD85289 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 80
ID ADD73821 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 81
ID ADD74559 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 82
ID ADD77087 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 83
ID ADD85781 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 84
ID ADE05330 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 85
ID ADD74805 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 86
ID ADG05617 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 87
ID ADG27171 standard; protein; 598 AA.
DE Human PRO polypeptide #52.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3135; DB 8; Length 598;
RESULT 88
ID ADG11234 standard; protein; 598 AA.
DE Novel human secreted and transmembrane protein PRO357.
PN US2003096967-A1.
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PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 89  
ID ADG12013 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 90  
ID ADP94570 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 91  
ID ADG66666 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 92  
ID ADG63481 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003211570-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 93  
ID ADH39010 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 94  
ID ADH43210 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2003207401-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 95  
ID ADG34100 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 96  
ID ADI33570 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2003096960-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 97  
ID ADH69664 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2004019183-A1.  
PD 29-JAN-2004.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 98  
ID ADI29825 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2003096961-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 99  
ID ADM27222 standard; protein; 598 AA.  
DE Novel human secreted and transmembrane protein PRO357.  
PN US2004044179-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 100  
ID ADK66580 standard; protein; 598 AA.  
DE Human PRO polypeptide #52.  
PN US2004044180-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 101  
ID ADN00448 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2004091972-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 102  
ID ADU25372 standard; protein; 598 AA.  
DE Human secreted/transmembrane PRO polypeptide #12.  
PN US2004220385-A1.  
PD 04-NOV-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 8; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 103  
ID ADI39535 standard; protein; 598 AA.  
DE Human insulin-like growth factor homolog PRO357 precursor protein.  
PN US2005048613-A1.  
PD 03-MAR-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 9; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 104  
ID ADY73816 standard; protein; 598 AA.  
DE Human PRO357 protein, SEQ ID NO: 69.  
PN US2005059115-A1.  
PD 17-MAR-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3135; DB 9; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4e-190;  
RESULT 105  
ID AAY17831 standard; protein; 598 AA.  
DE Human PRO357 protein sequence.  
PN WO9928462-A2.  
PD 10-JUN-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 99.7%; Score 3126; DB 2; Length 598;  
Best Local Similarity 99.8%; Pred. No. 1.5e-189;  
RESULT 106  
ID AAB07428 standard; protein; 673 AA.  
DE Amino acid sequence of a leucine-rich surface glycoprotein (LRSG).  
PN WO200042170-A1.  
PD 20-JUL-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.



Query Match 98.4%; Score 3083.5; DB 3; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 107  
ID AAB87533 standard; protein; 673 AA.  
DE Human PRO1282.  
PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 4; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 108  
ID AAB65166 standard; protein; 673 AA.  
DE Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 4; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 109  
ID AAU75266 standard; protein; 673 AA.  
DE Human Slit-like protein #1.  
PN WO200212346-A2.  
PD 14-FEB-2002.  
PA (PHAA ) PHARMACIA CORP.  
Query Match 98.4%; Score 3083.5; DB 5; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 110  
ID ABG95858 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 5; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 111  
ID ABG78042 standard; protein; 673 AA.  
DE Human leucine-rich surface glycoprotein (LRSG-1).  
PN US2002072089-A1.  
PD 13-JUN-2002.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (MACB/) MACBETH K J.  
PA (BUSF/) BUSFIELD S J.  
PA (PANY/) PAN Y.  
PA (WHIT/) WHITE D.  
PA (KHOD/) KHODADOUST M M.  
PA (GUWW/) GU W.  
Query Match 98.4%; Score 3083.5; DB 5; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 112  
ID ABUS7981 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 113  
ID ABUS9059 standard; protein; 673 AA.  
DE Novel human secreted or transmembrane protein PRO1282.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 114  
ID ABUS2571 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 115  
ID ABUS60490 standard; protein; 673 AA.

DE Human secreted/transmembrane protein, #19.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 116  
ID ABU13872 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 117  
ID ABU72457 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 118  
ID ABU90883 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 119  
ID ABO33942 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 120  
ID ABU71959 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 121  
ID ABU71513 standard; protein; 673 AA.  
DE Human secreted polypeptide PRO1282.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 122  
ID ABU72294 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 123  
ID ABU90967 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003018158-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 124  
ID ABUS9206 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein, #19.



PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 125  
ID ABO25903 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 126  
ID ABO27288 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO1282.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 127  
ID ABO2483 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 128  
ID ABO1153 standard; protein; 673 AA.  
DE Human secreted polypeptide PRO1282.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 129  
ID ABO3268 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 130  
ID ABO58912 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein, #19.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 131  
ID ABO92290 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 132  
ID ABO59355 standard; protein; 673 AA.  
DE Novel human secreted or transmembrane protein PRO1282.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 133  
ID ABO98270 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
ID ABO17073 standard; protein; 673 AA.

Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 134  
ID ABO9275 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 135  
ID ABO82482 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 136  
ID ABO92121 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 137  
ID ABO96446 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 138  
ID ABO10827 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 139  
ID ABO1579 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 140  
ID ABO72116 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 141  
ID ABO88518 standard; protein; 673 AA.  
DE Human secreted and transmembrane polypeptide PRO1282.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 142  
ID ABO34032 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 143  
ID ABO17073 standard; protein; 673 AA.



DE Human transmembrane PRO polypeptide (SeqID 16).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 144  
ID ADA37563 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 145  
ID ADA21249 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO1282.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 146  
ID ABO44246 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO 1282.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 147  
ID ADA10036 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein, PRO1282.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 148  
ID ADA19878 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 149  
ID ADB17261 standard; protein; 673 AA.  
DE Human transmembrane PRO polypeptide (SeqID 16).  
PN US2003050485-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 150  
ID ADA17580 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 151  
ID ADA27688 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 152  
ID ADA20050 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 153  
ID ABO34174 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO 1282.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 154  
ID ADA94268 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 155  
ID ADA38493 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 156  
ID ADA92614 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 157  
ID ADA00347 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO 1282.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 6; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 158  
ID ABO53118 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 159  
ID ADA22175 standard; protein; 673 AA.  
DE Human secreted/transmembrane polypeptide PRO1282.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 160  
ID ABO22488 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 161  
ID ADA06341 standard; protein; 673 AA.  
DE Human secreted/transmembrane PRO polypeptide #13.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 162  
ID ADA39034 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;



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RESULT 163
ID ADB85589 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 164
ID ADB96060 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 165
ID ADB68268 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 166
ID ADB68075 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 167
ID ADB90892 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 168
ID ADC57532 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 169
ID ADC54896 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 170
ID ADC11763 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 171
ID ADC06972 standard; protein; 673 AA.
DE Human PRO1282 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 172
ID ADC56185 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 173
ID ADC17151 standard; protein; 673 AA.
DE Mammalian PRO polypeptide (SeqID 16).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 174
ID ADC07240 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 175
ID ADC11230 standard; protein; 673 AA.
DE Human secreted/transmembrane protein PRO1282.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 176
ID ADC14849 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 177
ID ADC52344 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 178
ID ADC14352 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 179
ID ADD07884 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003086623-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 180
ID ADC81709 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 181
ID ADD07351 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 182
ID ADC82242 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003059833-A1.
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PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 183  
ID ADD08422 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 184  
ID ADD06671 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 185  
ID ADC82918 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 186  
ID ADD55025 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 187  
ID ADD36020 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 188  
ID ADD55983 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 189  
ID ADD54421 standard; protein; 673 AA.  
DE Human PRO polypeptide #13.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 190  
ID ADE26575 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 191  
ID ADE26042 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 192  
ID ADF66979 standard; protein; 673 AA.  
DE Human PRO1282 amino acid sequence SEQ ID NO:52.  
PN US2002198148-A1.

PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 193  
ID ADG01021 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 194  
ID ADG08574 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 195  
ID ADF95195 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 196  
ID ADH24048 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 197  
ID ADH34074 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 198  
ID ADH29907 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 199  
ID ADH23878 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 200  
ID ADG85282 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 201  
ID ADH24558 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180907-A1.  
PD 25-SEP-2003.



PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 202  
ID ADH37414 standard; protein; 673 AA.  
DE Human secreted and transmembrane protein PRO1282.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 203  
ID ADH02003 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 204  
ID ADH37584 standard; protein; 673 AA.  
DE Human secreted and transmembrane protein PRO1282.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 205  
ID ADG85622 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 206  
ID ADH24218 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 207  
ID ADH38512 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 208  
ID ADG83633 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 209  
ID ADH29441 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 210  
ID ADH27557 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 211  
ID ADH37754 standard; protein; 673 AA.  
DE Human secreted and transmembrane protein PRO1282.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 212  
ID ADH37931 standard; protein; 673 AA.  
DE Human secreted and transmembrane protein PRO1282.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 213  
ID ADH57351 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 214  
ID ADH53493 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 215  
ID ADH53663 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 216  
ID ADH51999 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 217  
ID ADH49854 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 218  
ID ADI25364 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 219  
ID ADH90157 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;



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Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 220
ID ADI2534 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 221
ID ADH97708 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 222
ID ADH97708 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 223
ID ADI35233 standard; protein; 673 AA.
DE Human PRO polypeptide #13.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 224
ID ADI35233 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 225
ID ADI11913 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 226
ID ADH89987 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 227
ID ADH9725 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 228
ID ADH98388 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 229
ID ADI11063 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 230
ID ADH98218 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 231
ID ADH98558 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 232
ID ADH98048 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 233
ID ADI05036 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 234
ID ADI03386 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 235
ID ADI04781 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 236
ID ADH78235 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 237
ID ADI19579 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 238
ID ADH90327 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
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PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 239
ID ADI03046 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 240
ID ADH77895 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 241
ID ADH97878 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 242
ID ADI01263 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 243
ID ADI01958 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 244
ID ADI03216 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 245
ID ADI11403 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 246
ID ADI02305 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 247
ID ADI11743 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003181665-A1.
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PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 248
ID ADI05380 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 249
ID ADH79452 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 250
ID ADI19409 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 251
ID ADI05210 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 252
ID ADH79622 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 253
ID ADI01448 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 254
ID ADI01618 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 255
ID ADI01788 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 7; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 256
ID ADH79792 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003191289-A1.
PD 09-OCT-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 257  
ID ADI04610 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 258  
ID ADI02746 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 259  
ID ADH78065 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 260  
ID ADI25704 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 261  
ID ADI25874 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 262  
ID ADK65386 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 263  
ID ADH98728 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 264  
ID ADH79969 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 265  
ID ADL93700 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.

Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 266  
ID ADC52154 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 267  
ID ADF35178 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 268  
ID ADG11428 standard; protein; 673 AA.  
DE Human PRO1282 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 269  
ID ADH06586 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 270  
ID ADH06416 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 271  
ID ADG68837 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 272  
ID ADH27727 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 273  
ID ADH25068 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 274  
ID ADH33700 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;



RESULT 275  
ID ADH02343 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 276  
ID ADH07950 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 277  
ID ADG69347 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 278  
ID ADH39168 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 279  
ID ADG83908 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 280  
ID ADH19298 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 281  
ID ADG8452 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 282  
ID ADH06246 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 283  
ID ADH30076 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 284

ID ADH24388 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 285  
ID ADG69517 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 286  
ID ADH07780 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 287  
ID ADG85792 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 288  
ID ADH39338 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 289  
ID ADH33530 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 290  
ID ADH33870 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 291  
ID ADH01080 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 292  
ID ADG69687 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 293  
ID ADH20791 standard; protein; 673 AA.



DE Human secreted/transmembrane protein PRO1282.  
PN US20032243358-A1.  
PD 04-DEC-2003.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 294  
ID ADH02173 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 295  
ID ADG69177 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 296  
ID ADG85962 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 297  
ID ADH24898 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 298  
ID ADH39515 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 299  
ID ADH19831 standard; protein; 673 AA.  
DE Human secreted/transmembrane protein PRO1282.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 300  
ID ADH02513 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 301  
ID ADG69007 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 302  
ID ADH07610 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180850-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 303  
ID ADG86132 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 304  
ID ADH24728 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 305  
ID ADH25776 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 306  
ID ADH38342 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 307  
ID ADH57181 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 308  
ID ADH52169 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 309  
ID ADH49535 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 310  
ID ADH90497 standard; protein; 673 AA.  
DE Novel human secreted and transmembrane protein PRO1282.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 98.4%; Score 3083.5; DB 8; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 311  
ID ADI11233 standard; protein; 673 AA.  
DE Human PRO polypeptide #8.  
PN US2003181683-A1.  
PD 25-SEP-2003.



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PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 312
ID ADH98898 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 313
ID ADI02128 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 314
ID ADH90667 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 315
ID ADJ98542 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181797-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 316
ID ADJ98712 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 317
ID ADH78871 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 318
ID ADJ99105 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 319
ID ADJ99275 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 320
ID ADJ98893 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 321
ID ADH79041 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 322
ID ADK00901 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 323
ID ADK14422 standard; protein; 673 AA.
DE Novel human secreted and transmembrane protein PRO1282.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 324
ID ADM80871 standard; protein; 673 AA.
DE Human PRO polypeptide #8.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 325
ID ADR45587 standard; protein; 673 AA.
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #1.
PN US2004176296-A1.
PD 09-SEP-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 98.4%; Score 3083.5; DB 8; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 326
ID ADY77711 standard; protein; 673 AA.
DE Neoplastic disease detection protein PRO1282.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERE/) GERITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 327
ID AEA38367 standard; protein; 673 AA.
DE Human secreted/transmembrane protein, #81.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 9; Length 673;
Best Local Similarity 88.7%; Pred. No. 8.5e-187;
RESULT 328
ID AEF12542 standard; protein; 673 AA.
DE Human PRO1282 protein SEQ ID NO:16.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH ) GENENTECH INC.
Query Match 98.4%; Score 3083.5; DB 10; Length 673;
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Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 329  
ID AEF74231 standard; protein; 673 AA.  
DE Human PRO1282 protein SEQ ID NO:16.  
PN US2005260647-A1.  
PD 24-NOV-2005.  
PA (EATC/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERK/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W L.  
Query Match 98.4%; Score 3083.5; DB 10; Length 673;  
Best Local Similarity 88.7%; Pred. No. 8.5e-187;  
RESULT 330  
ID AAB84689 standard; protein; 673 AA.  
DE Amino acid sequence of human slit polypeptide Zslit3.  
PN WO200148418-A1.  
PD 28-JUN-2001.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 98.2%; Score 3078.5; DB 4; Length 673;  
Best Local Similarity 88.6%; Pred. No. 1.8e-186;  
RESULT 331  
ID ADF69108 standard; protein; 673 AA.  
DE Human MP53 protein sequence SEQ ID NO:78.  
PN WO2003083047-A2.  
PD 09-OCT-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 98.2%; Score 3078.5; DB 7; Length 673;  
Best Local Similarity 88.6%; Pred. No. 1.8e-186;  
RESULT 332  
ID ABO59449 standard; protein; 676 AA.  
DE Human genome derived single exon protein #5683.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 98.2%; Score 3078.5; DB 8; Length 676;  
Best Local Similarity 88.6%; Pred. No. 1.8e-186;  
RESULT 333  
ID ADA57213 standard; protein; 672 AA.  
DE Human secreted protein #496.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 6; Length 672;  
Best Local Similarity 85.2%; Pred. No. 2.2e-177;  
RESULT 334  
ID ADA41092 standard; protein; 672 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 6; Length 672;  
Best Local Similarity 85.2%; Pred. No. 2.2e-177;  
RESULT 335  
ID ABR47923 standard; protein; 672 AA.  
DE Human secreted protein, SEQ ID 814.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 6; Length 672;  
Best Local Similarity 85.2%; Pred. No. 2.2e-177;  
RESULT 336  
ID AAB38323 standard; protein; 673 AA.  
DE Human secreted protein encoded by gene 3 clone HSYAV50.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 93.6%; Score 2935; DB 3; Length 673;  
Best Local Similarity 85.2%; Pred. No. 2.2e-177;  
RESULT 337  
ID AAB38400 standard; peptide; 723 AA.  
DE Fragment of human secreted protein encoded by gene 3 clone HSYAV50.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 93.6%; Score 2935; DB 3; Length 723;  
Best Local Similarity 85.2%; Pred. No. 2.4e-177;  
RESULT 338  
ID AAU75267 standard; protein; 630 AA.  
DE Human Slit-like protein #2.  
PN WO200212346-A2.  
PD 14-FEB-2002.  
PA (PHAA) PHARMACIA CORP.  
Query Match 90.8%; Score 2845.5; DB 5; Length 630;  
Best Local Similarity 85.2%; Pred. No. 9.4e-172;  
RESULT 339  
ID AAY66643 standard; protein; 611 AA.  
DE Membrane-bound protein PRO1282.  
PN WO9963088-A1.  
PD 09-DEC-1999.  
PA (GETH) GENENTECH INC.  
Query Match 86.5%; Score 2712.5; DB 3; Length 611;  
Best Local Similarity 79.5%; Pred. No. 2.4e-163;  
RESULT 340  
ID ABG78046 standard; protein; 673 AA.  
DE Mouse leucine-rich surface glycoprotein (LRSG-1).  
PN US2002072089-A1.  
PD 13-JUN-2002.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (MACB/) MACBETH K J.  
PA (BUSF/) BUSFIELD S J.  
PA (PANY/) PAN Y.  
PA (WHIT/) WHITE D.  
PA (KHOD/) KHODADOUST M M.  
PA (GUWW/) GU W.  
Query Match 79.4%; Score 2490; DB 5; Length 673;  
Best Local Similarity 73.5%; Pred. No. 3.4e-149;  
RESULT 341  
ID ADR45596 standard; protein; 673 AA.  
DE Human leucine-rich surface glycoprotein, LRSG-1, protein #2.  
PN US2004176296-A1.  
PD 09-SEP-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 79.4%; Score 2490; DB 8; Length 673;  
Best Local Similarity 73.5%; Pred. No. 3.4e-149;  
RESULT 342  
ID ADA00753 standard; protein; 673 AA.  
DE Murine stromal cell derived haematopoietin factor-5 SEQ ID NO:10.  
PN WO2003018805-A1.  
PD 06-MAR-2003.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
PA (NINA-) JAPAN NAT CANCER CENT.  
Query Match 79.2%; Score 2484; DB 6; Length 673;  
Best Local Similarity 73.4%; Pred. No. 8.1e-149;  
RESULT 343  
ID AAB07431 standard; protein; 493 AA.  
DE A leucine-rich surface glycoprotein (LRSG).  
PN WO200042170-A1.  
PD 20-JUL-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 53.3%; Score 1672; DB 3; Length 493;  
Best Local Similarity 53.3%; Pred. No. 1.6e-97;  
RESULT 344  
ID ABB72324 standard; protein; 281 AA.  
DE Rat protein isolated from skin cells SEQ ID NO: 648.  
PN WO200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 37.6%; Score 1178.5; DB 5; Length 281;



Best Local Similarity 80.7%; Pred. No. 1.5e-66;  
RESULT 345  
ID AAO30403 standard; protein; 311 AA.  
DE Human secreted protein (SECP)-6.  
PN WO2003046196-A1.  
PD 05-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 31.8%; Score 997.5; DB 7; Length 311;  
Best Local Similarity 68.7%; Pred. No. 4.9e-55;  
RESULT 346  
ID ABR58506 standard; protein; 307 AA.  
DE Human secreted protein Incyte ID No: 7500228CD1 SEQ ID NO: 18.  
PN WO2003029437-A2.  
PD 10-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 31.3%; Score 980.5; DB 6; Length 307;  
Best Local Similarity 67.9%; Pred. No. 5.8e-54;  
RESULT 347  
ID AAO30821 standard; protein; 117 AA.  
DE Human cell adhesion and extracellular matrix protein (CADECM)-11.  
PN WO2003047526-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 15.0%; Score 471; DB 7; Length 117;  
Best Local Similarity 98.9%; Pred. No. 3.5e-22;  
RESULT 348  
ID AAE23980 standard; protein; 635 AA.  
DE Human LP220 secreted protein.  
PN WO200226801-A2.  
PD 04-APR-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 11.5%; Score 360.5; DB 5; Length 635;  
Best Local Similarity 27.1%; Pred. No. 2.6e-14;  
RESULT 349  
ID ABP70142 standard; protein; 647 AA.  
DE Human NOV44a.  
PN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 11.5%; Score 360.5; DB 5; Length 647;  
Best Local Similarity 27.1%; Pred. No. 2.6e-14;  
RESULT 350  
ID AAO26256 standard; protein; 635 AA.  
DE MDDT related human protein SEQ ID No 34.  
PN WO200296951-A1.  
PD 05-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 11.5%; Score 359.5; DB 6; Length 635;  
Best Local Similarity 27.6%; Pred. No. 3e-14;  
RESULT 351  
ID AD209859 standard; protein; 635 AA.  
DE Human breast cancer marker MGC3103 protein.  
PN EP1522594-A2.  
PD 13-APR-2005.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 11.5%; Score 359.5; DB 9; Length 635;  
Best Local Similarity 27.6%; Pred. No. 3e-14;  
RESULT 352  
ID ABP70144 standard; protein; 778 AA.  
DE Human NOV44c.  
PN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 11.4%; Score 357.5; DB 5; Length 778;  
Best Local Similarity 26.7%; Pred. No. 5e-14;  
RESULT 353  
ID ADM90979 standard; protein; 545 AA.  
DE Human pharmaceutically useful protein SeqID 372.  
PN WO2004020595-A2.  
PD 11-MAR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.  
PA (DNAP-) DNAPFORM KK.

Query Match 11.2%; Score 350.5; DB 8; Length 545;  
Best Local Similarity 27.9%; Pred. No. 9.2e-14;  
RESULT 354  
ID ABP70143 standard; protein; 566 AA.  
DE Human NOV44b.  
PN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.8%; Score 339; DB 5; Length 566;  
Best Local Similarity 26.9%; Pred. No. 5.1e-13;  
RESULT 355  
ID AAE17484 standard; protein; 551 AA.  
DE Human leucine-rich repeat-8 (ZLRR8) protein #2.  
PN WO200202604-A2.  
PD 10-JAN-2002.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 10.8%; Score 338; DB 5; Length 551;  
Best Local Similarity 27.4%; Pred. No. 5.8e-13;  
RESULT 356  
ID ADI21104 standard; protein; 618 AA.  
DE Novel human protein #79.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.7%; Score 337; DB 7; Length 618;  
Best Local Similarity 27.2%; Pred. No. 7.6e-13;  
RESULT 357  
ID ADA23287 standard; protein; 653 AA.  
DE Human SECX polypeptide, SECS #1.  
PN US2003054514-A1.  
PD 20-MAR-2003.  
PA (SHIM/) SHIMKETS R A.  
PA (LARO/) LAROCHELLE W J.  
Query Match 10.7%; Score 337; DB 6; Length 653;  
Best Local Similarity 23.6%; Pred. No. 8.1e-13;  
RESULT 358  
ID AAB23033 standard; protein; 694 AA.  
DE Human SLIT protein-like splice variant, SECX 3352358-1.  
PN WO200053742-A2.  
PD 14-SEP-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.7%; Score 337; DB 3; Length 694;  
Best Local Similarity 23.6%; Pred. No. 8.7e-13;  
RESULT 359  
ID AAB23034 standard; protein; 590 AA.  
DE Human SLIT protein-like splice variant, SECX 3352358-2.  
PN WO200053742-A2.  
PD 14-SEP-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.6%; Score 333; DB 3; Length 590;  
Best Local Similarity 25.8%; Pred. No. 1.3e-12;  
RESULT 360  
ID ADA23289 standard; protein; 590 AA.  
DE Human SECX polypeptide, SEC6.  
PN US2003054514-A1.  
PD 20-MAR-2003.  
PA (SHIM/) SHIMKETS R A.  
PA (LARO/) LAROCHELLE W J.  
Query Match 10.6%; Score 333; DB 6; Length 590;  
Best Local Similarity 25.8%; Pred. No. 1.3e-12;  
RESULT 361  
ID AAG04827 standard; protein; 526 AA.  
DE Novel human diagnostic protein #4818.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.6%; Score 332; DB 4; Length 526;  
Best Local Similarity 26.9%; Pred. No. 1.3e-12;  
RESULT 362  
ID AAY28806 standard; protein; 653 AA.  
DE CG359.4 secreted protein.  
PN WO9950405-A1.  
PD 07-OCT-1999.



PA (GEM) GENETICS INST INC.  
 Query Match 10.5%; Score 330; DB 2; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 363  
 ID AAY66694 standard; protein; 653 AA.  
 DE Membrane-bound protein PRO1111.  
 PN WO963088-A2.  
 PD 09-DEC-1999.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 3; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 364  
 ID AAB24073 standard; protein; 653 AA.  
 DE Human PRO1111 protein sequence SEQ ID NO:46.  
 PN WO200053755-A2.  
 PD 14-SEP-2000.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 3; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 365  
 ID AAU12390 standard; protein; 653 AA.  
 DE Human PRO1111 polypeptide sequence.  
 PN WO200140466-A2.  
 PD 07-JUN-2001.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 4; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 366  
 ID AAQ09438 standard; protein; 653 AA.  
 DE Human sbgPRO331a protein.  
 PN WO200160850-A1.  
 PD 23-AUG-2001.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 PA (SMIK) SMITHKLINE BEECHAM PLC.  
 Query Match 10.5%; Score 330; DB 4; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 367  
 ID AAB5217 standard; protein; 653 AA.  
 DE Human PRO1111 (UNQ554) protein sequence SEQ ID NO:229.  
 PN WO200073454-A1.  
 PD 07-DEC-2000.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 4; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 368  
 ID ABUS8032 standard; protein; 653 AA.  
 DE Human PRO polypeptide #64.  
 PN US2003027163-A1.  
 PD 06-FEB-2003.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 369  
 ID ABUS9110 standard; protein; 653 AA.  
 DE Novel human secreted or transmembrane protein PRO1111.  
 PN US2002132252-A1.  
 PD 19-SEP-2002.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 370  
 ID ABUS9257 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein PRO1111.  
 PN US2003032023-A1.  
 PD 13-FEB-2003.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 371  
 ID ABO17834 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003032156-A1.  
 PD 13-FEB-2003.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 372  
 ID ABUS9869 standard; protein; 653 AA.  
 DE Novel secreted and transmembrane protein PRO1111.  
 PN US2003017563-A1.  
 PD 23-JAN-2003.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 373  
 ID ABUS9223 standard; protein; 653 AA.  
 DE Human PRO1111 polypeptide.  
 PN US2002103125-A1.  
 PD 01-AUG-2002.  
 PA (GEM) GENENTECH LTD.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 374  
 ID ABUS1088 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003004311-A1.  
 PD 02-JAN-2003.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 375  
 ID ABUS72508 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003003531-A1.  
 PD 02-JAN-2003.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 376  
 ID ABUS66788 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003036180-A1.  
 PD 20-FEB-2003.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 377  
 ID AAO231105 standard; protein; 653 AA.  
 DE NAG14 'human modifier of p53 pathway' protein.  
 PN WO2003035833-A2.  
 PD 01-MAY-2003.  
 PA (EXEL-) EXELIXIS INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 378  
 ID ABUS9869 standard; protein; 653 AA.  
 DE Novel secreted and transmembrane protein PRO1111.  
 PN US2003017563-A1.  
 PD 23-JAN-2003.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 379  
 ID ABUS9257 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein, #93.  
 PN US2003027162-A1.  
 PD 06-FEB-2003.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 380  
 ID ABO25954 standard; protein; 653 AA.  
 DE Human PRO1111 polypeptide.  
 PN US2002127576-A1.  
 PD 12-SEP-2002.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 381  
 ID ABO25954 standard; protein; 653 AA.  
 DE Human PRO1111 polypeptide.  
 PN US2002127576-A1.  
 PD 12-SEP-2002.  
 PA (GEM) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;



ID ABO25059 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein (PRO) #219.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 382  
ID ABUS8963 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein, #93.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 383  
ID ABU92341 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 384  
ID ABUS9406 standard; protein; 653 AA.  
DE Novel human secreted or transmembrane protein PRO1344.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 385  
ID ABU67064 standard; protein; 653 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 438.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 386  
ID ABU92172 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 387  
ID ABU10878 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 388  
ID ABU81630 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 389  
ID ABU88569 standard; protein; 653 AA.  
DE Human secreted and transmembrane polypeptide PRO1111.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 390  
ID ABO34083 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 391  
ID ADA45957 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 392  
ID ADA76388 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 393  
ID ADA19038 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 394  
ID ADA61661 standard; protein; 653 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 395  
ID ADB19446 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003088796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 396  
ID ADB27987 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 397  
ID ADA86466 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 398  
ID ADB16030 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 399  
ID ADA37740 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;



Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 400  
ID ADA47816 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 401  
ID ADA21426 standard; protein; 653 AA.  
DE Human secreted/transmembrane polypeptide PRO1111.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 402  
ID ADA10213 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein, PRO1111.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 403  
ID ADA67611 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 404  
ID ADB30618 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 405  
ID ADA85914 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 406  
ID ADA17757 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 407  
ID ADA97126 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 408  
ID ADA79430 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 409  
ID ADA87569 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003044945-A1.  
PD 06-MAR-2003.

PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 410  
ID ADB16771 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 411  
ID ADA27865 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 412  
ID ADA31863 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 413  
ID ADB14926 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 414  
ID ADB18887 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 415  
ID ADA94102 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 416  
ID ADB19998 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 417  
ID ADB13310 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 6; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 418  
ID ABO43367 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003044945-A1.  
PD 06-MAR-2003.



PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 419  
 ID ADA94445 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein PRO1111.  
 PN US2003059832-A1.  
 PD 27-MAR-2003.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 420  
 ID ADA74564 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003068798-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 421  
 ID ADB24797 standard; protein; 653 AA.  
 DE Human PRO polypeptide SEQ ID NO 438.  
 PN US200307713-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 422  
 ID ADA82321 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082701-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 423  
 ID ADA75284 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003073216-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 424  
 ID ADA8362 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003082695-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 425  
 ID ADA84810 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003082708-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 426  
 ID ADB30066 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003073214-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 427  
 ID ADA80594 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082761-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 428  
 ID ADA75836 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082703-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 429  
 ID ADA38670 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein PRO1111.  
 PN US2003059780-A1.  
 PD 27-MAR-2003.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 430  
 ID ADA47061 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003073210-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 431  
 ID ADB25357 standard; protein; 653 AA.  
 DE Human PRO polypeptide SEQ ID NO 438.  
 PN US200307715-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 432  
 ID ADA93533 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US200307721-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 433  
 ID ADB26883 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003092147-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 434  
 ID ADB31170 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003096386-A1.  
 PD 22-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 435  
 ID ADA92791 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein PRO1111.  
 PN US2003060407-A1.  
 PD 27-MAR-2003.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 436  
 ID ADA61098 standard; protein; 653 AA.  
 DE Homo sapiens.  
 PN US2003049817-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 437  
 ID ADB24245 standard; protein; 653 AA.



DE Human PRO polypeptide SEQ ID NO 438.  
 PN US200307714-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 438  
 ID ADA96574 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082690-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 439  
 ID ADA81146 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082702-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 440  
 ID ADA96022 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082759-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 441  
 ID ADB26331 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082760-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 442  
 ID ADB21816 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003082765-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 6; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 443  
 ID ADA77595 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003068797-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 444  
 ID ADB18335 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US200307710-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 445  
 ID ADA87018 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003082709-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 446  
 ID ADA88121 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.

PN US2003082700-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 447  
 ID ADA46509 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003054516-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 448  
 ID ADB28539 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082699-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 449  
 ID ADB29091 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082706-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 450  
 ID ABO53169 standard; protein; 653 AA.  
 DE Human secreted/transmembrane protein PRO1111.  
 PN US2003044806-A1.  
 PD 06-MAR-2003.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 451  
 ID ADA77043 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003059909-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 452  
 ID ADA22352 standard; protein; 653 AA.  
 DE Human secreted/transmembrane polypeptide PRO1111.  
 PN US2003040473-A1.  
 PD 27-FEB-2003.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 453  
 ID ADA88673 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003073213-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 454  
 ID ADA97678 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003082686-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 455  
 ID ADB27435 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003022339-A1.  
 PD 30-JAN-2003.  
 Query Match 10.5%; Score 330; DB 7; Length 653;



Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 456  
ID ADB22368 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 457  
ID ABO22539 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 458  
ID ADA06518 standard; protein; 653 AA.  
DE Human secreted/transmembrane PRO polypeptide #64.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 459  
ID ADA39211 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 460  
ID ADA67059 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 461  
ID ADB22920 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US200307711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 462  
ID ADB23693 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 463  
ID ADA92415 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 464  
ID ADB15478 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 465  
ID ADB38730 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082766-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 466  
ID ADB96237 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 467  
ID ADB38178 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 468  
ID ADB66650 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 469  
ID ADB89730 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 470  
ID ADB90462 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082782-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 471  
ID ADB35563 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 472  
ID ADB47186 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 473  
ID ADB86793 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 474  
ID ADB77398 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.



Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 475  
ID ADB34555 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 476  
ID ADB35659 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 477  
ID ADB34003 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 478  
ID ADB35107 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 479  
ID ADB36211 standard; protein; 653 AA.  
DE Human PRO polypeptide SEQ ID NO 438.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 480  
ID ADB46606 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 481  
ID ADC57709 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 482  
ID ADC55073 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 483  
ID ADC11940 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 484  
ID ADC56362 standard; protein; 653 AA.

DE Human PRO polypeptide #64.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 485  
ID ADC07417 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 486  
ID ADC11407 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein PRO1111.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 487  
ID ADC50479 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 488  
ID ADC72026 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 489  
ID ADC69005 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 490  
ID ADC33012 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 491  
ID ADC57366 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 492  
ID ADC57366 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein Seq ID438.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 493  
ID ADC51032 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;



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Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 494
ID ADC65559 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 495
ID ADC54657 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 496
ID ADC53618 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 497
ID ADC59141 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 498
ID ADC56019 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 499
ID ADC58589 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein Seq ID438.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 500
ID ADC14529 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 501
ID ADD08061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 502
ID ADD03263 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 503
ID ADC90255 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 504
ID ADC81896 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 505
ID ADC69674 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 506
ID ADC48563 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 507
ID ADD10092 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 508
ID ADD07528 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 509
ID ADD04667 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 510
ID ADC82419 standard; protein; 653 AA.
DE Human PRO polypeptide #64.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 511
ID ADC80623 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.5%; Score 330; DB 7; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 512
ID ADD11130 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194774-A1.
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PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 513  
ID ADC48011 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 514  
ID ADD08599 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 515  
ID ADC80071 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 516  
ID ADD06848 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 517  
ID ADD09540 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 518  
ID ADC83095 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 519  
ID ADD41253 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003030438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 520  
ID ADD52392 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 521  
ID ADD53132 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 522  
ID ADD53684 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 523  
ID ADD55202 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 524  
ID ADD56160 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 525  
ID ADD51840 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 526  
ID ADD02639 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 527  
ID ADD02073 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 528  
ID ADD54255 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 529  
ID ADD54598 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 530  
ID ADD92572 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 531  
ID ADD91468 standard; protein; 653 AA.



DE Human PRO polypeptide #219.  
 PN US2003199055-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 532  
 ID ADE04082 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003199057-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 533  
 ID ADE26752 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003087304-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 534  
 ID ADE32379 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003194765-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 535  
 ID ADE22311 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003199056-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 536  
 ID ADD79535 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003203428-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 537  
 ID ADE42071 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003194772-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 538  
 ID ADE17888 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003199023-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 539  
 ID ADD92020 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003199053-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 540  
 ID ADE33483 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003194767-A1.

PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 541  
 ID ADE34035 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003194791-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 542  
 ID ADD80087 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003207417-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 543  
 ID ADD93124 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003194768-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 544  
 ID ADE19544 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003199025-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 545  
 ID ADE18992 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003199026-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 546  
 ID ADE43188 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003199033-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 547  
 ID ADD95977 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003199059-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 548  
 ID ADE22863 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003199064-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 549  
 ID ADD78981 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003203429-A1.  
 PD 30-OCT-2003.



PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 550  
ID ADE26219 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 551  
ID ADE32931 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 552  
ID ADE42623 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199032-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 553  
ID ADD80639 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207418-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 554  
ID ADD89667 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 555  
ID ADE40951 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 556  
ID ADE04750 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 557  
ID ADE92879 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 558  
ID ADF67156 standard; protein; 653 AA.  
DE Human PRO1111 amino acid sequence SEQ ID NO:229.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;

Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 559  
ID ADG21588 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 560  
ID ADG23229 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 561  
ID ADF97564 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 562  
ID ADG80628 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 563  
ID ADG80076 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 564  
ID ADH55368 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 565  
ID ADH55920 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 566  
ID ADI35410 standard; protein; 653 AA.  
DE Human PRO polypeptide #64.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 567  
ID ADI64139 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 7; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 568



ID ADI5088 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003207386-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 569  
 ID ADI63587 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003207387-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 570  
 ID ADH82001 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003207388-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 571  
 ID ADH99902 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003049682-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 572  
 ID ADH81449 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003207377-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 573  
 ID ADM82618 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003087355-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 574  
 ID ADN16017 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003087353-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 575  
 ID ADN16646 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003087385-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 576  
 ID ADN15465 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003087356-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 577  
 ID ADN14913 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.

PN US2003087357-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 7; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 578  
 ID ADC81175 standard; protein; 653 AA.  
 DE Novel human secreted and transmembrane protein PRO1111.  
 PN US2003092115-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 8; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 579  
 ID ADD76623 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003100087-A1.  
 PD 29-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 8; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 580  
 ID ADD87987 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003092113-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 8; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 581  
 ID ADD86391 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003203440-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 8; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 582  
 ID ADE75839 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003211571-A1.  
 PD 13-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 8; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 583  
 ID ADE23415 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003092108-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 8; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 584  
 ID ADE23967 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003092110-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 8; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 585  
 ID ADE24610 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003092111-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.5%; Score 330; DB 8; Length 653;  
 Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
 RESULT 586  
 ID ADD87435 standard; protein; 653 AA.  
 DE Human PRO polypeptide #219.  
 PN US2003203439-A1.



PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 587  
ID ADE89301 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US200319062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 588  
ID ADE18440 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 589  
ID ADE88749 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US200319054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 590  
ID ADE94769 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US200319027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 591  
ID ADE91180 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US200319061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 592  
ID ADF35355 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 593  
ID ADE95321 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US200319052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 594  
ID ADE93431 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US200319060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 595  
ID ADF35012 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US200319029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 596  
ID ADE92327 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US200319051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 597  
ID ADE90628 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US200319063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 598  
ID ADE91775 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US200319058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 599  
ID ADG11605 standard; protein; 653 AA.  
DE Human PRO1111 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 600  
ID ADG02354 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 601  
ID ADG22140 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 602  
ID ADG20210 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 603  
ID ADF98116 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 604  
ID ADG24333 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;



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Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 605
ID ADF98687 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 606
ID ADG03518 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 607
ID ADF99239 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 608
ID ADG16824 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 609
ID ADG05283 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 610
ID ADG19550 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 611
ID ADG13387 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 612
ID ADG08444 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 613
ID ADG15614 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;

Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 614
ID ADF97012 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 615
ID ADG06197 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 616
ID ADG23781 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 617
ID ADG04070 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 618
ID ADG24971 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 619
ID ADG07268 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 620
ID ADG07820 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 621
ID ADG55315 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 622
ID ADG60979 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 623
ID ADG60979 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
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ID ADG62083 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 624
ID ADG82284 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 625
ID ADG57523 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 626
ID ADG56971 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 627
ID ADG55867 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 628
ID ADG58627 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 629
ID ADG70993 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 630
ID ADG58075 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 631
ID ADG53659 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 632
ID ADG71545 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207378-A1.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 633
ID ADG81732 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 634
ID ADH19475 standard; protein; 653 AA.
DE Human secreted/transmembrane protein PRO1111.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 635
ID ADH30694 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 636
ID ADH12061 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 637
ID ADG52483 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 638
ID ADG54211 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 639
ID ADG81180 standard; protein; 653 AA.
DE Human PRO polypeptide #219.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 640
ID ADG56419 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 330; DB 8; Length 653;
Best Local Similarity 24.3%; Pred. No. 2.3e-12;
RESULT 641
ID ADH12685 standard; protein; 653 AA.
DE Novel human secreted and transmembrane protein PRO1111.
PN US2003207378-A1.
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Query Match	10.5%;	Score 330;	DB 8;	Length 653;
Best Local Similarity	24.3%;	Pred. No. 2.3e-12;		
RESULT 651				
ID ADG99318 standard; protein; 653 AA.				
DE Novel human secreted and transmembrane protein PRO1111.				
PN US2004009547-A1.				
PD 15-JAN-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	10.5%;	Score 330;	DB 8;	Length 653;
Best Local Similarity	24.3%;	Pred. No. 2.3e-12;		
RESULT 652				
ID ADI14773 standard; protein; 653 AA.				
DE Novel human secreted and transmembrane protein PRO1111.				
PN US2003207383-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	10.5%;	Score 330;	DB 8;	Length 653;
Best Local Similarity	24.3%;	Pred. No. 2.3e-12;		
RESULT 653				
ID ADI18368 standard; protein; 653 AA.				
DE Novel human secreted and transmembrane protein PRO1111.				
PN US2003207349-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	10.5%;	Score 330;	DB 8;	Length 653;
Best Local Similarity	24.3%;	Pred. No. 2.3e-12;		
RESULT 654				
ID ADJ63649 standard; protein; 653 AA.				
DE Novel human secreted and transmembrane protein PRO1111.				
PN US2004039164-A1.				
PD 26-FEB-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	10.5%;	Score 330;	DB 8;	Length 653;
Best Local Similarity	24.3%;	Pred. No. 2.3e-12;		
RESULT 655				
ID ADJ77544 standard; protein; 653 AA.				
DE Human PRO polypeptide #219.				
PN US2004038336-A1.				
PD 26-FEB-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	10.5%;	Score 330;	DB 8;	Length 653;
Best Local Similarity	24.3%;	Pred. No. 2.3e-12;		
RESULT 656				
ID ADJ65666 standard; protein; 653 AA.				
DE Human PRO polypeptide #219.				
PN US2004038335-A1.				
PD 26-FEB-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	10.5%;	Score 330;	DB 8;	Length 653;
Best Local Similarity	24.3%;	Pred. No. 2.3e-12;		
RESULT 657				
ID ADM27802 standard; protein; 653 AA.				
DE Human PRO polypeptide #219.				
PN US2004048333-A1.				
PD 11-MAR-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	10.5%;	Score 330;	DB 8;	Length 653;
Best Local Similarity	24.3%;	Pred. No. 2.3e-12;		
RESULT 658				
ID ADM42526 standard; protein; 653 AA.				
DE Human PRO polypeptide #219.				
PN US2004058424-A1.				
PD 25-MAR-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	10.5%;	Score 330;	DB 8;	Length 653;
Best Local Similarity	24.3%;	Pred. No. 2.3e-12;		
RESULT 659				
ID ADM28388 standard; protein; 653 AA.				
DE Human PRO polypeptide #219.				
PN US2004077064-A1.				
PD 22-APR-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	10.5%;	Score 330;	DB 8;	Length 653;
Best Local Similarity	24.3%;	Pred. No. 2.3e-12;		
RESULT 660				
ID ADM28388 standard; protein; 653 AA.				
DE Human PRO polypeptide #219.				
PN US2004077064-A1.				
PD 22-APR-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	10.5%;	Score 330;	DB 8;	Length 653;
Best Local Similarity	24.3%;	Pred. No. 2.3e-12;		



Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 660  
ID ADI95870 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 661  
ID ADI96422 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 662  
ID ADS32374 standard; protein; 653 AA.  
DE Novel human secreted and transmembrane protein PRO1111.  
PN US2004203125-A1.  
PD 14-OCT-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 663  
ID ADT03358 standard; protein; 653 AA.  
DE Human PRO polypeptide #219.  
PN US2004214269-A1.  
PD 28-OCT-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 8; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 664  
ID ADZ03409 standard; protein; 653 AA.  
DE Human secreted/transmembrane PRO1111 protein.  
PN US2005074837-A1.  
PD 07-APR-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 665  
ID AEA38492 standard; protein; 653 AA.  
DE Human secreted/transmembrane protein, #132.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 666  
ID AEA23332 standard; protein; 653 AA.  
DE Tumor antigen of hematopoietic origin TAO15.  
PN WO2005049075-A2.  
PD 02-JUN-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 667  
ID AEB14155 standard; protein; 653 AA.  
DE Cancer cell diagnosis method-related human protein - SEQ ID 438.  
PN US2005153396-A1.  
PD 14-JUL-2005.  
PA (BAKE/) BAKER K P.  
PA (BERE/) BERESINI M.  
PA (DEFO/) DEFORGE L.  
PA (DESN/) DESNOYERS L.  
PA (FILV/) FILVAROFF E.  
PA (GAOW/) GAO W.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (SHER/) SHERWOOD S.

PA (SMIT/) SMITH V.  
PA (STEW/) STEWART T A.  
PA (TUNA/) TUNAS D.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
PA (ZHAN/) ZHANG Z.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 668  
ID AED86353 standard; protein; 653 AA.  
DE Human PRO amino acid sequence, seq id 438.  
PN US2005245730-A1.  
PD 03-NOV-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 330; DB 9; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 669  
ID AEF79019 standard; protein; 653 AA.  
DE Human NAG14 polypeptide SEQ ID NO: 2.  
PN US2006035826-A1.  
PD 16-FEB-2006.  
PA (LINJ/) LIN J C.  
PA (ROSE/) ROSENTHAL A.  
Query Match 10.5%; Score 330; DB 10; Length 653;  
Best Local Similarity 24.3%; Pred. No. 2.3e-12;  
RESULT 670  
ID ABU12069 standard; protein; 775 AA.  
DE Human NOV15a CG92531-01 protein SEQ ID 58.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.5%; Score 329.5; DB 6; Length 775;  
Best Local Similarity 26.0%; Pred. No. 3e-12;  
RESULT 671  
ID ABG98014 standard; protein; 649 AA.  
DE Human leucine rich repeat domain protein associated protein #1.  
PN WO200274959-A2.  
PD 26-SEP-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 10.5%; Score 329; DB 5; Length 649;  
Best Local Similarity 24.6%; Pred. No. 2.6e-12;  
RESULT 672  
ID ADS98753 standard; protein; 824 AA.  
DE Protein factor discovery related human contig polypeptide, SEQ ID 1017.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
PA (DRMA/) DRMANAC R T.  
Query Match 10.5%; Score 329; DB 8; Length 824;  
Best Local Similarity 25.5%; Pred. No. 3.4e-12;  
RESULT 673  
ID ABG34079 standard; protein; 627 AA.  
DE Human PRO peptide #51.  
PN WO200224888-A2.  
PD 28-MAR-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 5; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 674  
ID ADA01368 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003068779-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 6; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 675  
ID ADA43797 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003064474-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 6; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;



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Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 676
ID ADA43565 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 6; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 677
ID ADA01240 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 678
ID ADA01124 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 679
ID ADA43681 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 680
ID ADA06943 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 681
ID ADA08431 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 682
ID ADB99724 standard; protein; 627 AA.
DE Human PRO polypeptide SEQ ID 100.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 683
ID ADB87007 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 684
ID ADB66162 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 685
ID ADB99840 standard; protein; 627 AA.
DE Human PRO polypeptide SEQ ID 100.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 686
ID ADB99495 standard; protein; 627 AA.
DE Novel human secreted and transmembrane protein PRO34192.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 687
ID ADB66046 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 688
ID ADC23444 standard; protein; 627 AA.
DE Human transmembrane PRO polypeptide (SeqID 100).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 689
ID ADC26137 standard; protein; 627 AA.
DE Human PRO34192 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 690
ID ADE04964 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 691
ID ADE11270 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 692
ID ADD88201 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 693
ID ADD95496 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.5%; Score 328.5; DB 7; Length 627;
Best Local Similarity 24.2%; Pred. No. 2.7e-12;
RESULT 694
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ID ADE06426 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003073195-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 695  
ID ADE38201 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119120-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 696  
ID ADE88317 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003073189-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 697  
ID ADE30898 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003073188-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 698  
ID ADF99453 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003078401-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 699  
ID ADG06546 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003077742-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 700  
ID ADG05497 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003077741-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 701  
ID ADG82498 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003077744-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 7; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 702  
ID ADE51751 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104560-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 703  
ID ADE51867 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.

DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104561-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 704  
ID ADE37725 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104564-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 705  
ID ADE37609 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104565-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 706  
ID ADD95380 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003138901-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 707  
ID ADE38080 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003104566-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 708  
ID ADE76169 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003124665-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 709  
ID ADE39492 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119117-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 710  
ID ADE04296 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003096364-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 711  
ID ADE39893 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003138896-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 712  
ID ADE19758 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.



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PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 713
ID ADE77336 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 714
ID ADE65444 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 715
ID ADE76053 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 716
ID ADE37964 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 717
ID ADE64574 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 718
ID ADE38909 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 719
ID ADE51983 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 720
ID ADD91014 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 721
ID ADE38793 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003108996-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 722
ID ADE37493 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 723
ID ADE06309 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 724
ID ADD90169 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 725
ID ADE38677 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 726
ID ADE39608 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 727
ID ADD89213 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 728
ID ADD88980 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 729
ID ADE19874 standard; protein; 627 AA.
DE Human PRO polypeptide #50.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC. 10.5%; Score 328.5; DB 8; Length 627;
Query Match 24.2%; Pred. No. 2.7e-12;
Best Local Similarity
RESULT 730
ID ADE77452 standard; protein; 627 AA.
DE Human secreted/transmembrane polypeptide PRO34192.
PN US2003124667-A1.
PD 03-JUL-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 731  
ID ADE65328 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119113-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 732  
ID ADE39376 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119115-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 733  
ID ADE38561 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003104559-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 734  
ID ADG11114 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003170809-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 735  
ID ADG10998 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003077743-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 736  
ID ADH31526 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119139-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 737  
ID ADH38774 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119140-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 738  
ID ADH29409 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119137-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 739  
ID ADH23712 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 740  
ID ADH27042 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119135-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 741  
ID ADH38310 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119124-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 742  
ID ADH26926 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119134-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 743  
ID ADH38194 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119123-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 744  
ID ADH38890 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119141-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 745  
ID ADH23828 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119142-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 746  
ID ADH40203 standard; protein; 627 AA.  
DE Human PRO34192 protein.  
PN US2003119132-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 747  
ID ADH40088 standard; protein; 627 AA.  
DE Human PRO34192 protein.  
PN US2003119133-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 748  
ID ADH31410 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003119138-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 749  
ID ADH23712 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003119143-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.



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Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 749  
ID ADH29288 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane polypeptide PRO34192.  
PN US2003119136-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 750  
ID ADH49503 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 751  
ID ADH51967 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 752  
ID ADH49822 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 753  
ID ADH52423 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 754  
ID ADH52539 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 755  
ID ADH58536 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 756  
ID ADH51851 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 757  
ID ADH58412 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 758  
ID ADI13609 standard; protein; 627 AA.  
DE Novel human secreted and transmembrane protein PRO34192.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 759  
ID ADK00865 standard; protein; 627 AA.  
DE Human PRO polypeptide #50.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 760  
ID ADI08606 standard; protein; 627 AA.  
DE Human secreted/transmembrane polypeptide PRO34192.  
PN US2003186372-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.5%; Score 328.5; DB 8; Length 627;  
Best Local Similarity 24.2%; Pred. No. 2.7e-12;  
RESULT 761  
ID AAU32870 standard; protein; 636 AA.  
DE Novel human secreted protein #361.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.4%; Score 327.5; DB 4; Length 636;  
Best Local Similarity 24.2%; Pred. No. 3.2e-12;  
RESULT 762  
ID ABO84499 standard; protein; 626 AA.  
DE Mouse cancer-associated protein MP14-035.1.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.3%; Score 324; DB 8; Length 626;  
Best Local Similarity 24.3%; Pred. No. 5.2e-12;  
RESULT 763  
ID AAG85805 standard; protein; 628 AA.  
DE Human leucine-rich repeat (LRR) family member, 33395 polypeptide.  
PN WO200172827-A2.  
PD 04-OCT-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.3%; Score 324; DB 4; Length 628;  
Best Local Similarity 24.1%; Pred. No. 5.2e-12;  
RESULT 764  
ID ADN95165 standard; protein; 810 AA.  
DE Human BEC/LEC-related protein sequence SeqID87.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
Query Match 10.3%; Score 322.5; DB 7; Length 810;  
Best Local Similarity 22.0%; Pred. No. 8.7e-12;  
RESULT 765  
ID ABR58642 standard; protein; 811 AA.  
DE Human cancer related protein SEQ ID NO:299.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.3%; Score 322.5; DB 6; Length 811;  
Best Local Similarity 22.0%; Pred. No. 8.7e-12;  
RESULT 766  
ID AAO23114 standard; protein; 811 AA.  
DE KIAA0644 'human modifier of p53 pathway' protein.  
PN WO2003035833-A2.  
PD 01-MAY-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 10.3%; Score 322.5; DB 6; Length 811;  
Best Local Similarity 22.0%; Pred. No. 8.7e-12;



RESULT 767  
ID ADN95110 standard; protein; 811 AA.  
DE Human LEC protein sequence SeqID32.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN-) LICENTIA LTD.  
Query Match 10.3%; Score 322.5; DB 7; Length 811;  
Best Local Similarity 22.0%; Pred. No. 8.7e-12;  
RESULT 768  
ID ADQ21196 standard; protein; 811 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4016.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 10.3%; Score 322.5; DB 8; Length 811;  
Best Local Similarity 22.0%; Pred. No. 8.7e-12;  
RESULT 769  
ID ADR45590 standard; protein; 605 AA.  
DE Homologue of LRSG-1, baboon ALS.  
PN US2004176296-A1.  
PD 09-SEP-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.3%; Score 322; DB 8; Length 605;  
Best Local Similarity 36.2%; Pred. No. 6.6e-12;  
RESULT 770  
ID AAG67523 standard; protein; 628 AA.  
DE Amino acid sequence of a human secreted polypeptide.  
PN WO200166690-A2.  
PD 13-SEP-2001.  
PA (SMIK-) SMITHKLINE BEECHAM CORP.  
PA (SMIK-) SMITHKLINE BEECHAM PLC.  
Query Match 10.2%; Score 321; DB 4; Length 628;  
Best Local Similarity 23.9%; Pred. No. 8e-12;  
RESULT 771  
ID AAB84469 standard; protein; 628 AA.  
DE Amino acid sequence of an interferon omega-1 like protein NOV2.  
PN WO200142471-A2.  
PD 14-JUN-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.2%; Score 321; DB 4; Length 628;  
Best Local Similarity 23.9%; Pred. No. 8e-12;  
RESULT 772  
ID ABP69326 standard; protein; 628 AA.  
DE Human polypeptide SEQ ID NO 1373.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.2%; Score 321; DB 5; Length 628;  
Best Local Similarity 23.9%; Pred. No. 8e-12;  
RESULT 773  
ID ADF69107 standard; protein; 628 AA.  
DE Human MP53 protein sequence SEQ ID NO:77.  
PN WO2003083047-A2.  
PD 09-OCT-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 10.2%; Score 321; DB 7; Length 628;  
Best Local Similarity 23.9%; Pred. No. 8e-12;  
RESULT 774  
ID ADH71652 standard; protein; 628 AA.  
DE Human protein of the invention NOV22a SEQ ID NO:548.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.2%; Score 321; DB 8; Length 628;  
Best Local Similarity 23.9%; Pred. No. 8e-12;  
RESULT 775  
ID ADH71654 standard; protein; 628 AA.  
DE Human protein of the invention NOV22b SEQ ID NO:550.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 10.2%; Score 321; DB 8; Length 628;

Best Local Similarity 23.9%; Pred. No. 8e-12;  
RESULT 776  
ID ABO84502 standard; protein; 628 AA.  
DE Human cancer-associated protein HP14-035.3.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.2%; Score 321; DB 8; Length 628;  
Best Local Similarity 23.9%; Pred. No. 8e-12;  
RESULT 777  
ID ABO84503 standard; protein; 628 AA.  
DE Human cancer-associated protein HP14-035.4.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.2%; Score 321; DB 8; Length 628;  
Best Local Similarity 23.9%; Pred. No. 8e-12;  
RESULT 778  
ID ABO84501 standard; protein; 628 AA.  
DE Human cancer-associated protein HP14-035.2.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.2%; Score 321; DB 8; Length 628;  
Best Local Similarity 23.9%; Pred. No. 8e-12;  
RESULT 779  
ID ABP70928 standard; protein; 762 AA.  
DE Human LP341 protein.  
PN WO2003029778-A2.  
PD 10-APR-2003.  
PA (ELIL-) LILLY & CO ELI.  
Query Match 10.2%; Score 321; DB 6; Length 762;  
Best Local Similarity 25.5%; Pred. No. 1e-11;  
RESULT 780  
ID ADI36917 standard; protein; 797 AA.  
DE Human LRR protein #12.  
PN US2003220263-A1.  
PD 27-NOV-2003.  
PA (FEDE-) FEDER J N.  
PA (MINT-) MINTIER G.  
PA (RAMA-) RAMANATHAN C S.  
Query Match 10.2%; Score 321; DB 8; Length 797;  
Best Local Similarity 25.5%; Pred. No. 1.1e-11;  
RESULT 781  
ID ADS98018 standard; protein; 803 AA.  
DE Protein factor discovery related isolated human polypeptide. SEQ ID 282.  
PN WO2004087874-A2.  
PD 14-OCT-2004.  
PA (NUVE-) NUVELO INC.  
PA (DRWA-) DRWANAC R T.  
Query Match 10.2%; Score 321; DB 8; Length 803;  
Best Local Similarity 25.5%; Pred. No. 1.1e-11;  
RESULT 782  
ID AAY13349 standard; protein; 660 AA.  
DE Amino acid sequence of protein PRO265.  
PN WO9914328-A2.  
PD 25-MAR-1999.  
PA (GETH-) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 2; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 783  
ID ADC78348 standard; protein; 660 AA.  
DE Human PRO265 protein.  
PN WO200015796-A2.  
PD 23-MAR-2000.  
PA (GETH-) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 3; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 784  
ID AAB80217 standard; protein; 660 AA.  
DE Human PRO265 protein.  
PN WO200104311-A1.  
PD 18-JAN-2001.



PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 4; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 785  
ID AAB31208 standard; protein; 660 AA.  
DE Amino acid sequence of human polypeptide PRO265.  
PN WO200077037-A2.  
PD 21-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 4; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 786  
ID AAU12346 standard; protein; 660 AA.  
DE Human PRO265 polypeptide sequence.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 4; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 787  
ID ABB84839 standard; protein; 660 AA.  
DE Human PRO265 protein sequence SEQ ID NO:46.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 5; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 788  
ID ABB95445 standard; protein; 660 AA.  
DE Human angiogenesis related protein PRO265 SEQ ID NO: 46.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
PA (BAKE//) BAKER K P.  
PA (FERR//) FERRARA N.  
PA (GERB//) GERBER H.  
PA (GERR//) GERRITSEN M E.  
PA (GODD//) GODDARD A.  
PA (GODO//) GODOWSKI P J.  
PA (GURN//) GURNEY A L.  
PA (HILL//) HILLAN K J.  
PA (MARS//) MARSTERS S A.  
PA (PANJ//) PAN J.  
PA (PAON//) PAONI N F.  
PA (STEP//) STEPHAN J F.  
PA (WATA//) WATANABE C K.  
PA (WILL//) WILLIAMS P M.  
PA (WOOD//) WOOD W I.  
Query Match 10.2%; Score 320; DB 5; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 789  
ID ABU71595 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 790  
ID AB017790 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 791  
ID ABU71450 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 792  
ID ABO25179 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 793  
ID ABU81044 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 794  
ID ABU71896 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein PRO265.  
PN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 795  
ID ABO01779 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 796  
ID ABU66744 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 797  
ID ABU54352 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein PRO265.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 798  
ID ABU67297 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 799  
ID AAO23116 standard; protein; 660 AA.  
DE FURT2 'human modifier of p53 pathway' protein.  
PN WO2003035833-A2.  
PD 01-MAY-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 800  
ID ABO47367 standard; protein; 660 AA.  
DE Human secreted/transmembrane polypeptide PRO265.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;



RESULT 801  
ID ABU59825 standard; protein; 660 AA.  
DE Novel secreted and transmembrane protein PRO265.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 802  
ID ABO25015 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein (PRO) #175.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 803  
ID ABU64504 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 804  
ID ABU72065 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2002177165-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 805  
ID ABU67350 standard; protein; 660 AA.  
DE Human secreted protein PRO265.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 806  
ID ABU67166 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003032062-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 807  
ID ABO14870 standard; protein; 660 AA.  
DE Human secreted / transmembrane polypeptide PRO265.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 808  
ID ABU67020 standard; protein; 660 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 350.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 809  
ID ABU69627 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003017463-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 810

ID ABU79808 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein PRO265.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 811  
ID ABO14809 standard; protein; 660 AA.  
DE Human secreted / transmembrane polypeptide PRO265.  
PN US2003027143-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 812  
ID ADA45869 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 813  
ID ADA76300 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 814  
ID ADB29233 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003092002-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 815  
ID ADA18950 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 816  
ID ADA61573 standard; protein; 660 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 817  
ID ADB19358 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 818  
ID ADB27899 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 6; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 819  
ID ADA86378 standard; protein; 660 AA.



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DE Novel human secreted and transmembrane protein PRO265.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 820
ID ADB15942 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 821
ID ADA47728 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 822
ID ADA18089 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 823
ID ABO32761 standard; protein; 660 AA.
DE Human secreted/transmembrane protein PRO265.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 824
ID ADA67523 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 825
ID ADB30530 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 826
ID ADA85826 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 827
ID ADA97038 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 828
ID ADA79342 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077722-A1.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 829
ID ADA87481 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 830
ID ADB16683 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 831
ID ABO34821 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 832
ID ADA16064 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 833
ID ADA91775 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 834
ID ADB14838 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 835
ID ADA47287 standard; protein; 660 AA.
DE Human secreted/transmembrane polypeptide PRO265.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 836
ID ADB18799 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 837
ID ADA94014 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077722-A1.
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PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 838
ID ADB19910 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 839
ID ADB13222 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 840
ID ABO43323 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 841
ID ADA74476 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003086798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 842
ID ADA42209 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 843
ID ADB24709 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 844
ID ADA82233 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 845
ID ADA75196 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 846
ID ADA85274 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 847
ID ADA84722 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 848
ID ABO17499 standard; protein; 660 AA.
DE Human PRO polypeptide #6.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 849
ID ADB29978 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 850
ID ADA80506 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 851
ID ADA75748 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 852
ID ADA46973 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 853
ID ADB25269 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 854
ID ADA93445 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match 10.2%; Score 320; DB 6; Length 660;
  Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 855
ID ADB26795 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
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Query Match      10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 856
ID ADB31082 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 857
ID ADA61010 standard; protein; 660 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 858
ID ADB24157 standard; protein; 660 AA.
DE Human PRO polypeptide SEQ ID NO 350.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 859
ID ADA96486 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 860
ID ADA81058 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 861
ID ADA95934 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 862
ID ADB26243 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 863
ID ADB21728 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 6; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 864
ID ADA77507 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 865
ID ADB18247 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 866
ID ADA86930 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 867
ID ADA16488 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 868
ID ADA12917 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 869
ID ADA41785 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 870
ID ADA88033 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 871
ID ADA46421 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 872
ID ADA17132 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 873
ID ADA42635 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 7; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
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RESULT 874  
ID ADB28451 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 875  
ID ADB29003 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 876  
ID ADA76955 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 877  
ID ADA8585 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 878  
ID ADA97590 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 879  
ID ADB27347 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003022339-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 880  
ID ADB22280 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 881  
ID ABO19866 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein PRO265.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 882  
ID ABO17560 standard; protein; 660 AA.  
DE Human PRO polypeptide #6.  
PN US2003064923-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 883  
ID ADA66971 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.

PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 884  
ID ADB2832 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003077111-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 885  
ID ADB23605 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US2003077112-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 886  
ID ADA92327 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 887  
ID ADB15390 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 888  
ID ADB38642 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 889  
ID ADB38090 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 890  
ID ADB66562 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 891  
ID ADB89642 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 892  
ID ADB90374 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082762-A1.



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PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 893  
ID ADB77554 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003077654-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 894  
ID ADB39475 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 895  
ID ADB74690 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003082542-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 896  
ID ADB47098 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 897  
ID ADB86705 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 898  
ID ADB77310 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 899  
ID ADB34467 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 900  
ID ADB35571 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 901  
ID ADB33915 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US2003077716-A1.  
PD 24-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 902  
ID ADB35019 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 903  
ID ADB36123 standard; protein; 660 AA.  
DE Human PRO polypeptide SEQ ID NO 350.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 904  
ID ADB46518 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 905  
ID ADC28336 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003059772-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 906  
ID ADC39536 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 907  
ID ADC40050 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 908  
ID ADC18878 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003036061-A1.  
PD 28-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 909  
ID ADC34174 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 910  
ID ADC29229 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.







RESULT 929  
ID ADC12272 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 930  
ID ADD03175 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 931  
ID ADC90167 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 932  
ID ADC69586 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 933  
ID ADC48475 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 934  
ID ADD10004 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 935  
ID ADD04579 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 936  
ID ADC80535 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 937  
ID ADD11042 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 938  
ID ADD52304 standard; protein; 660 AA.

ID ADD10335 standard; protein; 660 AA.  
DE Human secreted/transmembrane PRO polypeptide #23.  
PN US2003105011-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 939  
ID ADC47923 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 940  
ID ADD04827 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 941  
ID ADC79983 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 942  
ID ADD11295 standard; protein; 660 AA.  
DE Human secreted/transmembrane PRO polypeptide #23.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 943  
ID ADD09452 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 944  
ID ADD03833 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 945  
ID ADD03409 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 946  
ID ADD41165 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 947  
ID ADD52304 standard; protein; 660 AA.



DE Human PRO polypeptide #175.  
PN US2003194769-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 948  
ID ADD53044 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 949  
ID ADD53596 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 950  
ID ADD37088 standard; protein; 660 AA.  
DE Human secreted/transmembrane PRO polypeptide #23.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 951  
ID ADD51752 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 952  
ID ADD02551 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 953  
ID ADD01985 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 954  
ID ADD54167 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 955  
ID ADD92484 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 956  
ID ADD91380 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.

PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 957  
ID ADE03994 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 958  
ID ADE32291 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 959  
ID ADE22223 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 960  
ID ADD79447 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 961  
ID ADE41983 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 962  
ID ADE17800 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 963  
ID ADD91932 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 964  
ID ADE33395 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 965  
ID ADE33947 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003194791-A1.



PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 966  
 ID ADD79999 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003207417-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 967  
 ID ADD93036 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003194768-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 968  
 ID ADE19456 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003199025-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 969  
 ID ADE34661 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein, #7.  
 PN US2003077583-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 970  
 ID ADE18904 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003199026-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 971  
 ID ADE43100 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003199033-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 972  
 ID ADD95889 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003199059-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 973  
 ID ADE22775 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003199064-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 974  
 ID ADD78893 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003203429-A1.  
 PD 30-OCT-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 975  
 ID ADE32843 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003194766-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 976  
 ID ADE42535 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003199032-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 977  
 ID ADD80551 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003207418-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 978  
 ID ADD89579 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003199028-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 979  
 ID ADE40863 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003199031-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 980  
 ID ADE04662 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003199034-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 981  
 ID ADE92791 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003194777-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 982  
 ID ADG21500 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003207355-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 7; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 983  
 ID ADG23141 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003207384-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.



Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 984  
ID ADF97476 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 985  
ID ADG80540 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 986  
ID ADG79988 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 987  
ID ADG63796 standard; protein; 660 AA.  
DE Human secreted/transmembrane polypeptide PRO265.  
PN US2003170721-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 988  
ID ADH59144 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 989  
ID ADH55280 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 990  
ID ADH55832 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 991  
ID ADI37923 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 992  
ID ADI65000 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;

Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 993  
ID ADI63499 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 994  
ID ADH81913 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 995  
ID ADH81361 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 996  
ID ADJ26191 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 997  
ID ADM82530 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 998  
ID ADNI5929 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 999  
ID ADNI6558 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1000  
ID ADNI5377 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1001  
ID ADNI4825 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 7; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;







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DE Human PRO polypeptide #175.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1021
ID ADE99295 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1022
ID ADE94681 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1023
ID ADE91092 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1024
ID ADE95233 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1025
ID ADE93343 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1026
ID ADF34924 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1027
ID ADE98414 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1028
ID ADE92239 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO365.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1029
ID ADE90540 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1030
ID ADE91687 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1031
ID ADE98841 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1032
ID ADG40311 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GUEN/) GUERNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1033
ID ADF73705 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1034
ID ADG02266 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1035
ID ADG22052 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1036
ID ADG20122 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 10.2%; Score 320; DB 8; Length 660;
  Pred. No. 9.8e-12;
RESULT 1037
ID ADF98028 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1038
ID ADG24245 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1039
ID ADF98599 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1040
ID ADG03430 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1041
ID ADF9151 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1042
ID ADG16736 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1043
ID ADG05195 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1044
ID ADG19462 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1045
ID ADF73281 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1046
ID ADG13299 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1047
ID ADG08356 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1048
ID ADG15526 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1049
ID ADF96924 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1050
ID ADG06109 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1051
ID ADG23693 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1052
ID ADG03982 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1053
ID ADG24883 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1054
ID ADG07180 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1055
ID ADG07732 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
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RESULT 1056  
ID ADG55227 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1057  
ID ADG60891 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1058  
ID ADG61995 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1059  
ID ADG92124 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1060  
ID ADG82196 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1061  
ID ADG57435 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1062  
ID ADG56883 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1063  
ID ADG55779 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1064  
ID ADG58539 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1065  
ID ADG52395 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.

ID ADG70905 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1066  
ID ADG92551 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1067  
ID ADG57987 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1068  
ID ADG53571 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1069  
ID ADG71457 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1070  
ID ADG81644 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1071  
ID ADH30606 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1072  
ID ADG63645 standard; protein; 660 AA.  
DE Human secreted/transmembrane polypeptide PRO265.  
PN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1073  
ID ADH11973 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1074  
ID ADG52395 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.



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PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1075
ID ADG54123 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1076
ID ADG81092 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1077
ID ADG56331 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1078
ID ADH12597 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1079
ID ADG61443 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1080
ID ADH28530 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1081
ID AG54675 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1082
ID ADG59715 standard; protein; 660 AA.
DE Novel human secreted and transmembrane protein PRO265.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1083
ID ADH20340 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1084
ID ADH43479 standard; protein; 660 AA.
DE Human PRO polypeptide #23.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1085
ID ADH07195 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1086
ID ADH59740 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1087
ID ADH06768 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1088
ID ADI81139 standard; protein; 660 AA.
DE Human PRO polypeptide #175.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1089
ID ADI18510 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1090
ID ADI65230 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 8; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1091
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ID ADI37493 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003096340-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1092  
ID ADG09882 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1093  
ID ADH97297 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003190610-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1094  
ID ADI15353 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1095  
ID ADG09230 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1096  
ID ADI14685 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1097  
ID ADH60400 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2004023331-A1.  
PD 05-FEB-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOVSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1098  
ID ADI18280 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1099  
ID ADJ99457 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003187238-A1.

PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1100  
ID ADL08650 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003186358-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1101  
ID ADM24955 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1102  
ID ADJ63561 standard; protein; 660 AA.  
DE Novel human secreted and transmembrane protein PRO265.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1103  
ID ADM29741 standard; protein; 660 AA.  
DE Human secreted/transmembrane protein, #7.  
PN US2003190611-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1104  
ID ADJ77456 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1105  
ID ADK82824 standard; protein; 660 AA.  
DE Human PRO polypeptide #23.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1106  
ID ADJ65578 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1107  
ID ADM27714 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 10.2%; Score 320; DB 8; Length 660;  
Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
RESULT 1108  
ID ADM42438 standard; protein; 660 AA.  
DE Human PRO polypeptide #175.  
PN US2004058424-A1.  
PD 25-MAR-2004.



PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 8; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1109  
 ID ADO06063 standard; protein; 660 AA.  
 DE Human PRO polypeptide #6.  
 PN US6686451-B1.  
 PD 03-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 8; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1110  
 ID ADM28300 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2004077064-A1.  
 PD 22-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 8; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1111  
 ID ADRI0915 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein, #7.  
 PN US2004137561-A1.  
 PD 15-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 8; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1112  
 ID ADRI7824 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein, #7.  
 PN US2004147017-A1.  
 PD 29-JUL-2004.  
 PA (ASHK/) ASHKENAZI A.  
 PA (BOTS/) BOTSTEIN D.  
 PA (DESN/) DESNOYERS L.  
 PA (EATO/) EATON D L.  
 PA (FERR/) FERRARA N.  
 PA (FILV/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GRIM/) GRIMALDI C J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.  
 PA (MATH/) MATHER J P.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 10.2%; Score 320; DB 8; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1113  
 ID ADI95782 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2003077659-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 8; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1114  
 ID ADI96334 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2003207354-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 8; Length 660;

Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1115  
 ID ADI65657 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein, #7.  
 PN US2003148371-A1.  
 PD 07-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 8; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1116  
 ID ADS74463 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein #7.  
 PN US2004185531-A1.  
 PD 23-SEP-2004.  
 PA (ASHK/) ASHKENAZI A.  
 PA (BOTS/) BOTSTEIN D.  
 PA (DESN/) DESNOYERS L.  
 PA (EATO/) EATON D L.  
 PA (FERR/) FERRARA N.  
 PA (FILV/) FILVAROFF E.  
 PA (FONG/) FONG S.  
 PA (GAOW/) GAO W.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GRIM/) GRIMALDI C J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (KLJA/) KLJAVIN I J.  
 PA (MATH/) MATHER J P.  
 PA (PANJ/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (ROYM/) ROY M A.  
 PA (STEW/) STEWART T A.  
 PA (TUMA/) TUMAS D.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 Query Match 10.2%; Score 320; DB 8; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1117  
 ID ADS32286 standard; protein; 660 AA.  
 DE Novel human secreted and transmembrane protein PRO265.  
 PN US2004203125-A1.  
 PD 14-OCT-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 8; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1118  
 ID ADT03270 standard; protein; 660 AA.  
 DE Human PRO polypeptide #175.  
 PN US2004214269-A1.  
 PD 28-OCT-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 8; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1119  
 ID ADT03500 standard; protein; 660 AA.  
 DE Human secreted/transmembrane protein, #7.  
 PN US2003152922-A1.  
 PD 14-AUG-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 10.2%; Score 320; DB 8; Length 660;  
 Best Local Similarity 22.4%; Pred. No. 9.8e-12;  
 RESULT 1120  
 ID ADU06386 standard; protein; 660 AA.  
 DE Novel bronchial cancer-associated human protein SeqID610.  
 PN DE10316701-A1.  
 PD 04-NOV-2004.  
 PA (HINZ/) HINZMANN B.  
 PA (HERM/) HERMANN K.  
 PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
 Query Match 10.2%; Score 320; DB 8; Length 660;



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Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1121
ID ADZ03321 standard; protein; 660 AA.
DE Human secreted/transmembrane PRO265 protein.
PN US2005074837-A1.
PD 07-APR-2005.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1122
ID AEA37738 standard; protein; 660 AA.
DE Human secreted/transmembrane protein, #7.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1123
ID AEB14067 standard; protein; 660 AA.
DE Cancer cell diagnosis method-related human protein - SEQ ID 350.
PN US2005153396-A1.
PD 14-JUL-2005.
PA (BAKE/) BAKER K P.
PA (BERE/) BERESINI M.
PA (DEFO/) DEFORGE L.
PA (DESN/) DESNOYERS L.
PA (FILV/) FILVAROFF E.
PA (GAOW/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (SHER/) SHERWOOD S.
PA (SMIT/) SMITH V.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.
PA (ZHAN/) ZHANG Z.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1124
ID AED23772 standard; protein; 660 AA.
DE Human secreted protein PRO 265, SEQ ID 28.
PN US2005214904-A1.
PD 29-SEP-2005.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1125
ID AED86265 standard; protein; 660 AA.
DE Human PRO amino acid sequence, seq id 350.
PN US2005245730-A1.
PD 03-NOV-2005.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 9; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1126
ID AEG68941 standard; protein; 660 AA.
DE Fibromodulin homologous PRO265 protein, SEQ ID 28.
PN US6974689-B1.
PD 13-DEC-2005.
PA (GETH ) GENENTECH INC.
Query Match 10.2%; Score 320; DB 10; Length 660;
Best Local Similarity 22.4%; Pred. No. 9.8e-12;
RESULT 1127
ID ADT77808 standard; protein; 452 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP ) UNIV ROCHESTER.
Query Match 10.2%; Score 318.5; DB 8; Length 452;
Best Local Similarity 27.3%; Pred. No. 7.9e-12;
RESULT 1128
ID ADT77802 standard; protein; 452 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP ) UNIV ROCHESTER.
Query Match 10.2%; Score 318.5; DB 8; Length 452;
Best Local Similarity 27.8%; Pred. No. 1.5e-11;
RESULT 1129
ID AEF79023 standard; protein; 648 AA.
DE Mouse NAG14 polypeptide SEQ ID NO: 6.
PN US2006035826-A1.
PD 16-FEB-2006.
PA (LINJ/) LIN J C.
PA (ROSE/) ROSENTHAL A.
Query Match 10.1%; Score 317.5; DB 10; Length 648;
Best Local Similarity 24.2%; Pred. No. 1.4e-11;
RESULT 1130
ID AAE13006 standard; protein; 713 AA.
DE Human leucine-rich repeat (LRR) family member protein.
PN WO200175105-A2.
PD 11-OCT-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.1%; Score 317.5; DB 4; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.5e-11;
RESULT 1131
ID AAU91335 standard; protein; 713 AA.
DE Human novel secreted protein LP223(a).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 10.1%; Score 316.5; DB 5; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.8e-11;
RESULT 1132
ID ABG97991 standard; protein; 713 AA.
DE Human nervous system leucine rich repeat protein (HLRRNS1) #2.
PN WO200274959-A2.
PD 26-SEP-2002.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 10.1%; Score 316.5; DB 5; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.8e-11;
RESULT 1133
ID ABU52381 standard; protein; 713 AA.
DE Human GPCR related protein NOV31a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.1%; Score 316.5; DB 6; Length 713;
Best Local Similarity 23.1%; Pred. No. 1.8e-11;
RESULT 1134
ID ADT77796 standard; protein; 474 AA.
DE Chimeric Nogo receptor polypeptide.
PN WO2004090103-A2.
PD 21-OCT-2004.
PA (UYRP ) UNIV ROCHESTER.
Query Match 10.0%; Score 314.5; DB 8; Length 474;
Best Local Similarity 27.8%; Pred. No. 1.5e-11;
RESULT 1135
ID AAU91341 standard; protein; 656 AA.
DE Human novel secreted protein LP223(b).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 10.0%; Score 313.5; DB 5; Length 656;
Best Local Similarity 23.6%; Pred. No. 2.5e-11;
RESULT 1136
ID ADL24097 standard; protein; 713 AA.
DE Human NOVX polypeptide #71.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
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(SPVT/) SPYTEK K A.  
PA (PATT/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (MALY/) MALYANKAR U M.  
PA (BOLD/) BOLDOG F L.  
PA (GUOX/) GUO X.  
PA (SHEN/) SHENOY S G.  
PA (PADI/) PADIGARU M.  
PA (TAUP/) TAUPIER R J.  
PA (MILL/) MILLER C E.  
PA (CASM/) CASMAN S J.  
PA (PENA/) PENNA C E A.  
PA (GANG/) GANGOLLI E A.  
PA (GUSE/) GUSEV V Y.  
PA (SMIT/) SMITHSON G.  
PA (ZERR/) ZERHUSEN B D.  
PA (GERL/) GERLACH V.  
PA (POCH/) POCHART P F.  
PA (FERN/) FERNANDES E R.  
PA (SHIM/) SHIMKETS R A.  
PA (RAST/) RASTELLI L.  
PA (SPAD/) SPADERNA S K.  
PA (LARO/) LAROCHELLE W J.  
PA (ZHON/) ZHONG M.  
PA (KHRA/) KHRAMTSOV N V.  
PA (VOSS/) VOSS E Z.  
PA (HERR/) HERRMANN J L.  
Query Match  
Best Local Similarity 10.0%; Score 313.5; DB 8; Length 713;  
RESULT 1137  
ID AAE09437 standard; protein; 592 AA.  
DE Human sbgTango79a protein.  
PN WO200160850-A1.  
PD 23-AUG-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 4; Length 592;  
RESULT 1138  
ID AAE25351 standard; protein; 592 AA.  
DE Human Lp polypeptide, LP243.  
PN WO200248361-A2.  
PD 20-JUN-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;  
RESULT 1139  
ID AAU91329 standard; protein; 592 AA.  
DE Human novel secreted protein LP243 (b).  
PN WO200214358-A2.  
PD 21-FEB-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;  
RESULT 1140  
ID ABP60996 standard; protein; 592 AA.  
DE Novel human protein. SEQ ID 83.  
PN WO200250105-A1.  
PD 27-JUN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;  
RESULT 1141  
ID AAU79167 standard; protein; 592 AA.  
DE Human leucine-rich repeat proteins-like protein NOV4.  
PN WO200214368-A2.  
PD 21-FEB-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 5; Length 592;  
RESULT 1142  
ID ABG74693 standard; protein; 592 AA.  
DE Human CGDD protein 6803363CD1 SEQ ID 19.  
PN WO2003014322-A2.  
PD 20-FEB-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 6; Length 592;  
RESULT 1143  
ID ADE03417 standard; protein; 592 AA.  
DE Human immunoglobulin superfamily member BGS-2.  
PN US2003195163-A1.  
PD 16-OCT-2003.  
PA (WUSS/) WU S.  
PA (KRYG/) KRYSTEK S R.  
PA (LEEL/) LEE L.  
PA (FEDE/) FEDER J N.  
PA (CHEN/) CHENG J D.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 7; Length 592;  
RESULT 1144  
ID ADU02709 standard; protein; 592 AA.  
DE Novel human polypeptide seqid 1176.  
PN WO2004093804-A2.  
PD 04-NOV-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 8; Length 592;  
RESULT 1145  
ID ABG61770 standard; protein; 608 AA.  
DE Novel leucine-rich protein.  
PN WO200229058-A2.  
PD 11-APR-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 10.0%; Score 312; DB 5; Length 608;  
RESULT 1146  
ID ABG97967 standard; protein; 634 AA.  
DE Human nervous system leucine rich repeat protein (HLRRNS1) #1.  
PN WO200274959-A2.  
PD 26-SEP-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match  
Best Local Similarity 9.9%; Score 311; DB 5; Length 634;  
RESULT 1147  
ID ABR55628 standard; protein; 420 AA.  
DE Amino acid sequence of rat Nogo-66 receptor homologue NgrH1.  
PN WO2003035687-A1.  
PD 01-MAY-2003.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS PHARMA GMBH.  
Query Match  
Best Local Similarity 9.9%; Score 310.5; DB 6; Length 420;  
RESULT 1148  
ID ADT77788 standard; protein; 420 AA.  
DE Rat Nogo receptor 2 polypeptide.  
PN WO2004090103-A2.  
PD 21-OCT-2004.  
PA (UYRP ) UNIV ROCHESTER.  
Query Match  
Best Local Similarity 9.9%; Score 310.5; DB 8; Length 420;  
RESULT 1149  
ID AAO23115 standard; protein; 674 AA.  
DE FLRT1 'human modifier of p53 pathway' protein.  
PN WO2003035833-A2.  
PD 01-MAY-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match  
Best Local Similarity 9.9%; Score 310.5; DB 6; Length 674;  
RESULT 1150  
ID ADH17606 standard; protein; 674 AA.



DE Human NOV19a protein - SEQ ID 296.  
PN WO2003093432-A2.  
PD 13-NOV-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.9%; Score 310.5; DB 8; Length 674;  
Best Local Similarity 21.5%; Pred. No. 4e-11;  
RESULT 1151  
ID ADHI17628 standard; protein; 674 AA.  
DE Human NOV191 protein - SEQ ID 318.  
PN WO2003093432-A2.  
PD 13-NOV-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.9%; Score 310.5; DB 8; Length 674;  
Best Local Similarity 21.5%; Pred. No. 4e-11;  
RESULT 1152  
ID ADHI17630 standard; protein; 674 AA.  
DE Human NOV19m protein - SEQ ID 320.  
PN WO2003093432-A2.  
PD 13-NOV-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.9%; Score 310.5; DB 8; Length 674;  
Best Local Similarity 21.5%; Pred. No. 4e-11;  
RESULT 1153  
ID ADHI17634 standard; protein; 674 AA.  
DE Human NOV19o protein - SEQ ID 324.  
PN WO2003093432-A2.  
PD 13-NOV-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.9%; Score 310.5; DB 8; Length 674;  
Best Local Similarity 21.5%; Pred. No. 4e-11;  
RESULT 1154  
ID ADHI17632 standard; protein; 674 AA.  
DE Human NOV19n protein - SEQ ID 322.  
PN WO2003093432-A2.  
PD 13-NOV-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.9%; Score 310.5; DB 8; Length 674;  
Best Local Similarity 21.5%; Pred. No. 4e-11;  
RESULT 1155  
ID ABO27346 standard; protein; 585 AA.  
DE Human secreted/transmembrane polypeptide PRO1865.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 585;  
Best Local Similarity 22.3%; Pred. No. 4.2e-11;  
RESULT 1156  
ID ABO34232 standard; protein; 585 AA.  
DE Human secreted/transmembrane polypeptide PRO 1865.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 585;  
Best Local Similarity 22.3%; Pred. No. 4.2e-11;  
RESULT 1157  
ID AAU29215 standard; protein; 649 AA.  
DE Human PRO polypeptide sequence #192.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH-) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1158  
ID AAB70533 standard; protein; 649 AA.  
DE Human PRO3 protein sequence SEQ ID NO:6.  
PN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.9%; Score 309; DB 4; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1159  
ID AAB87591 standard; protein; 649 AA.  
DE Human PRO1865.

PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH-) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 4; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1160  
ID ABG95916 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein PRO1865.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH-) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 5; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1161  
ID ABH84953 standard; protein; 649 AA.  
DE Human PRO1865 protein sequence SEQ ID NO:274.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH-) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 5; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1162  
ID ABP70109 standard; protein; 649 AA.  
DE Human NOV27a.  
PN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 9.9%; Score 309; DB 5; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1163  
ID ABB95559 standard; protein; 649 AA.  
DE Human angiogenesis related protein PRO1865 SEQ ID NO: 274.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH-) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 9.9%; Score 309; DB 5; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1164  
ID ABU58591 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1165  
ID ABU88139 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1166  
ID ABU84454 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;



RESULT 1167  
 ID ABR66328 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003027278-A1.  
 PD 06-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1168  
 ID ABR65718 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003036159-A1.  
 PD 20-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1169  
 ID ABR99658 standard; protein; 649 AA.  
 DE Human secreted/transmembrane protein (PRO) #192.  
 PN US2003040070-A1.  
 PD 27-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1170  
 ID ABR62897 standard; protein; 649 AA.  
 DE Human PRO polypeptide #192.  
 PN US2003032113-A1.  
 PD 13-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1171  
 ID ABR90018 standard; protein; 649 AA.  
 DE Novel human secreted and transmembrane protein PRO1865.  
 PN US2003036147-A1.  
 PD 20-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1172  
 ID ABR68267 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003027264-A1.  
 PD 06-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1173  
 ID ABR96320 standard; protein; 649 AA.  
 DE Novel human secreted and transmembrane protein PRO1865.  
 PN US2003036144-A1.  
 PD 20-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1174  
 ID ABR92751 standard; protein; 649 AA.  
 DE Human secreted/transmembrane protein (PRO) #192.  
 PN US2003036149-A1.  
 PD 20-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1175  
 ID ABR08828 standard; protein; 649 AA.  
 DE Human secreted/transmembrane protein (PRO) #192.  
 PN US2003044923-A1.  
 PD 06-MAR-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1176  
 ID ABR02880 standard; protein; 649 AA.  
 DE Human secreted/transmembrane protein (PRO) #192.  
 PN US2003040062-A1.  
 PD 27-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1177  
 ID ABR75034 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003040056-A1.  
 PD 27-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1178  
 ID ABR94796 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003044926-A1.  
 PD 06-MAR-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1179  
 ID ABR65769 standard; protein; 649 AA.  
 DE Human PRO polypeptide #192.  
 PN US2003036140-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1180  
 ID ABR98929 standard; protein; 649 AA.  
 DE Novel human secreted and transmembrane protein PRO1865.  
 PN US2003013153-A1.  
 PD 16-JAN-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1181  
 ID ABR98144 standard; protein; 649 AA.  
 DE Novel human secreted and transmembrane protein PRO1865.  
 PN US2003017544-A1.  
 PD 23-JAN-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1182  
 ID ABR91850 standard; protein; 649 AA.  
 DE Novel human secreted and transmembrane protein PRO1865.  
 PN US2003027277-A1.  
 PD 06-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1183  
 ID ABR9543 standard; protein; 649 AA.  
 DE Human PRO polypeptide #192.  
 PN US2003036141-A1.  
 PD 20-FEB-2003.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1184  
 ID ABR6384 standard; protein; 649 AA.  
 DE Human secreted/transmembrane protein (PRO) #192.  
 PN US2003036146-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1185  
 ID ABR67597 standard; protein; 649 AA.  
 DE Human secreted/transmembrane protein (PRO) #192.  
 PN US2003036162-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1186  
 ID ABR0625 standard; protein; 649 AA.  
 DE Human PRO protein #192.  
 PN US2003036137-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
 22.3%; Pred. No. 4.8e-11;  
 RESULT 1187  
 ID ABR90941 standard; protein; 649 AA.



DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1188  
ID ABO34000 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein PRO1865.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1189  
ID ABR99543 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1190  
ID ABR98933 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040084-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1191  
ID ABO16456 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1192  
ID ABR92356 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1193  
ID ABO18997 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1194  
ID ABR78418 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1195  
ID ABUT2017 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1196  
ID ABUS154 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1197

ID ABO00293 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1198  
ID ABO11625 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1199  
ID ABO02270 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1200  
ID ABUS8844 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1201  
ID ABUS3539 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1202  
ID ABO06340 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1203  
ID ABR9376 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1204  
ID ABO09438 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1205  
ID ABO19302 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1206  
ID ABO11320 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1207  
ID ABR66938 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.



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PN US2003036148-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1208
ID ABO16151 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1209
ID ABO13857 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1210
ID ABU71571 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1211
ID ABU65760 standard; protein; 649 AA.
DE Human secreted/transmembrane protein, SEQ ID 384.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1212
ID ABO07608 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1213
ID ABO03795 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1214
ID ABR67243 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1215
ID ABO15846 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1216
ID ABU56127 standard; protein; 649 AA.
DE Human secreted/transmembrane protein, PRO1865.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1217
ID ABU72352 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2002182638-A1.
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PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1218
ID ABU65455 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1219
ID ABU95400 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1220
ID ABU71303 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1221
ID ABO07913 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1222
ID ABR70154 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1223
ID ABR69487 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1224
ID ABO01628 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1225
ID ABU81430 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1226
ID ABR60227 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match          9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1227
ID ABU91025 standard; protein; 649 AA.
DE Human PRO polypeptide #66.
PN US2003018168-A1.
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PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1228  
ID ABR67962 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1229  
ID ABR65350 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1230  
ID ABR68572 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1231  
ID ABR71984 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1232  
ID ABR85464 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1233  
ID ABR89154 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1234  
ID ABR83234 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1235  
ID ABR95090 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1236  
ID ABR90638 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1237  
ID ABR84149 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032111-A1.  
PD 13-FEB-2003.

Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1238  
ID ABR93800 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1239  
ID ABR65045 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027283-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1240  
ID ABR68877 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1241  
ID ABO06693 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1242  
ID ABR99238 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1243  
ID ABR57122 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1244  
ID ABR6074 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1245  
ID ABR2361 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1246  
ID ABR7372 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1247  
ID ABR83844 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1248  
ID ABR83844 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;



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RESULT 1248
ID ABO08218 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1249
ID ABU92541 standard; protein; 649 AA.
DE Human secreted/transmembrane protein PRO1865.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1250
ID ABU81929 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032104-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1251
ID ABU66093 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1252
ID ABU81211 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1253
ID ABR59922 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1254
ID ABU94110 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1255
ID ABU99963 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1256
ID ABR66633 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1257
ID ABR91051 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1258
ID ABO53325 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1259
ID ABU94478 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1260
ID ABU79360 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1261
ID ABU86689 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1262
ID ABU86994 standard; protein; 649 AA.
DE Novel human secreted and transmembrane protein PRO1865.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1263
ID ABU94783 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1264
ID ABO04710 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1265
ID ABR70459 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1266
ID ABU98624 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1267
ID ABR66023 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1268
ID ABR66023 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;

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ID ABR64740 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1269  
ID ABU79665 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1270  
ID ABU93056 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1271  
ID ABU96015 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1272  
ID ABU91235 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1273  
ID ABU90328 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1274  
ID ABO09743 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1275  
ID ABO11015 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1276  
ID ABR71069 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1277  
ID ABU98328 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1278  
ID ABU87677 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.

PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1279  
ID ABU91545 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1280  
ID ABU93333 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1281  
ID ABU84759 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1282  
ID ABR69849 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1283  
ID ABU80226 standard; protein; 649 AA.  
DE Human PRO protein #192.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1284  
ID ABU82540 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1285  
ID ABU93495 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1286  
ID ABO10048 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1287  
ID ABO09133 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1288  
ID ABU96504 standard; protein; 649 AA.  
DE Human PRO polypeptide #86.  
PN US2003027993-A1.



PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1289  
ID ABRU0701 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein #192.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1290  
ID ABRU72174 standard; protein; 649 AA.  
DE Human PRO polypeptide #66.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1291  
ID ABRU95710 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1292  
ID ABRU96919 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1293  
ID ABR70764 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1294  
ID ABO05115 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1295  
ID ABO08523 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1296  
ID ABO05730 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1297  
ID ABR74119 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1298  
ID ABR95711 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1299  
ID ABR81008 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1300  
ID ABR81313 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1301  
ID ABRM01009 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1302  
ID ABR88611 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003086743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1303  
ID ABRM77432 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1304  
ID ABO28916 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1305  
ID ABO31661 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1306  
ID ABRM08078 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1307  
ID ABO40558 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.



PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1308  
ID ABO35983 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1309  
ID ABO44122 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1310  
ID ADA78136 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1311  
ID ABM24917 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1312  
ID ABO03185 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1313  
ID ABR90441 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1314  
ID ABM17355 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054439-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1315  
ID ABR95101 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1316  
ID ABR95406 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1317  
ID ADB17189 standard; protein; 649 AA.  
DE Human transmembrane PRO polypeptide (SeqID 132).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1318  
ID ABO21644 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1319  
ID ABR97908 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1320  
ID ABR87696 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1321  
ID ABM77737 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1322  
ID ABM27967 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1323  
ID ABM06248 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1324  
ID ABM03754 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1325  
ID ABM35205 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1326  
ID ABM26442 standard; protein; 649 AA.



DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1327  
ID ABO48224 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1328  
ID ABR29366 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1329  
ID ABO24727 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1330  
ID ABM11738 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1331  
ID ABM02839 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1332  
ID ABM16135 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1333  
ID ABO27696 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1334  
ID ABM29187 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1335  
ID ABM07163 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.

PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Result 1336  
ID ABM21157 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Result 1337  
ID ABM09603 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Result 1338  
ID ABM041473 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Result 1339  
ID ABO36288 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Result 1340  
ID ABO43817 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Result 1341  
ID ABM76517 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Result 1342  
ID ABM76213 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Result 1343  
ID ABM25832 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Result 1344  
ID ABM26137 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;



Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1345  
ID ABO3490 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1346  
ID ABO2575 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1347  
ID ABO4304 standard; protein; 649 AA.  
DE Human secreted/transmembrane polypeptide PRO 1865.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1348  
ID ABR90746 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1349  
ID ABR73814 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1350  
ID ABO17066 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1351  
ID ABR94491 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1352  
ID ABR75998 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1353  
ID ABR71374 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1354  
ID ABR93271 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1355  
ID ABR93576 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1356  
ID ABR88001 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1357  
ID ABO30136 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1358  
ID ABO30136 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1359  
ID ABO33345 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1360  
ID ABM05033 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1361  
ID ABM08993 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1362  
ID ABO36593 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1363  
ID ABO35678 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.



Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1364  
 ID ABO39643 standard; protein; 649 AA.  
 DE Human secreted/transmembrane protein (PRO) #192.  
 PN US2003068776-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1365  
 ID ABM10518 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003069407-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1366  
 ID ABM12043 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003104555-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1367  
 ID ABO52189 standard; protein; 649 AA.  
 DE Human PRO polypeptide #192.  
 PN US2003049768-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1368  
 ID ABO52494 standard; protein; 649 AA.  
 DE Human PRO polypeptide #192.  
 PN US2003049771-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1369  
 ID ADA19994 standard; protein; 649 AA.  
 DE Novel human secreted and transmembrane protein PRO1865.  
 PN US2003069394-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1370  
 ID ABO23812 standard; protein; 649 AA.  
 DE Human secreted/transmembrane protein (PRO) #192.  
 PN US2003032134-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1371  
 ID ADB17377 standard; protein; 649 AA.  
 DE Human transmembrane PRO polypeptide (SeqID 132).  
 PN US2003050465-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1372  
 ID ABR97298 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003054481-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;

RESULT 1373  
 ID ABR87086 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003049778-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1374  
 ID ABM11128 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003049782-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1375  
 ID ABM28272 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003054476-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1376  
 ID ABO32271 standard; protein; 649 AA.  
 DE Human secreted/transmembrane protein (PRO) #192.  
 PN US2003068733-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1377  
 ID ABM15398 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003068692-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1378  
 ID ABM06553 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003068709-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1379  
 ID ABM04364 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003068716-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1380  
 ID ABM22477 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003068740-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1381  
 ID ABM07773 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003068751-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
 RESULT 1382  
 ID ABM07773 standard; protein; 649 AA.  
 DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
 PN US2003068751-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 9.9%; Score 309; DB 6; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 4.8e-11;







RESULT 1401  
ID ABM32968 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1402  
ID ABM22782 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1403  
ID ABM74993 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1404  
ID ADA79928 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1405  
ID ABR96383 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1406  
ID ABM02534 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1407  
ID ABR86476 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1408  
ID ABR86781 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003048772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1409  
ID ABM16745 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1410  
ID ABM29797 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064456-A1.  
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1411  
ID ABO29221 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1412  
ID ABM24002 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1413  
ID ABM23392 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1414  
ID ABM22172 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1415  
ID ABO37813 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1416  
ID ABM28577 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1417  
ID ABM28882 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1418  
ID ABM66526 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;  
RESULT 1419  
ID ABM75908 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
Pred. No. 4.8e-11;



RESULT 1420  
ID ABM34188 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 4.8e-11;  
RESULT 1421  
ID ABM34493 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 4.8e-11;  
RESULT 1422  
ID ABO20424 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 4.8e-11;  
RESULT 1423  
ID ABO211339 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 4.8e-11;  
RESULT 1424  
ID ABO22254 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
FN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 4.8e-11;  
RESULT 1425  
ID ADA20166 standard; protein; 649 AA.  
DE Novel human secreted and transmembrane protein PRO1865.  
FN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 4.8e-11;  
RESULT 1426  
ID ABR96688 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 4.8e-11;  
RESULT 1427  
ID ABR85866 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 4.8e-11;  
RESULT 1428  
ID ABR99848 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 4.8e-11;  
RESULT 1429  
ID ABW00399 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
FN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;  
22.3%; Pred. No. 4.8e-11;

PN US2003073172-A1. 9.9%; Score 309; DB 6; Length 649;  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1430  
ID ABM00704 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1431  
ID AB029831 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1432  
ID ABM23697 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1433  
ID ABM29492 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1434  
ID AB038423 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1435  
ID ABO45723 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1436  
ID ABM20647 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1437  
ID ADA81655 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1438  
ID ABO16761 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 9.9%; Score 309; DB 6; Length 649;



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Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1439
ID ABO18387 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1440
ID ABO22814 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003027285-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1441
ID ABO23119 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003054461-A1.
PD 20-MAR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1442
ID ABR92661 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064446-A1.
PD 03-APR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1443
ID ABR81618 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049744-A1.
PD 13-MAR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1444
ID ABR78042 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003049783-A1.
PD 13-MAR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1445
ID ABR89831 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1446
ID ABM26747 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1447
ID ABM13873 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003064458-A1.
PD 03-APR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1448
ID ABO28611 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064460-A1.
PD 13-MAR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1449
ID ABO30441 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003064464-A1.
PD 03-APR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1450
ID ABM07468 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068702-A1.
PD 10-APR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1451
ID ABM04059 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003068734-A1.
PD 10-APR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1452
ID ABO37203 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068719-A1.
PD 10-APR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1453
ID ABO41778 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003068729-A1.
PD 10-APR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1454
ID ABO35373 standard; protein; 649 AA.
DE Human PRO polypeptide #192.
PN US2003068738-A1.
PD 10-APR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1455
ID ABM25222 standard; protein; 649 AA.
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1456
ID ABO47614 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049742-A1.
PD 13-MAR-2003.
Query Match
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 9.9%; Score 309; DB 6; Length 649;
Best Local Similarity 22.3%; Pred. No. 4.8e-11;
RESULT 1457
ID ABO47919 standard; protein; 649 AA.
DE Human secreted/transmembrane protein (PRO) #192.
PN US2003049747-A1.
PD 13-MAR-2003.
Query Match
PA (GETH ) GENENTECH INC.
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Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1458  
ID ABO48529 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1459  
ID ABO51579 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1460  
ID ABO51884 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1461  
ID ABO50664 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1462  
ID ABR79788 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1463  
ID ABR17050 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1464  
ID ABO18082 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1465  
ID ABO21034 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1466  
ID ABR96993 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
ID ABR12348 standard; protein; 649 AA.

DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1468  
ID ABR16440 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1469  
ID ABR24307 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1470  
ID ABR14788 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1471  
ID ABR04669 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1472  
ID ABR06858 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1473  
ID ABR09298 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003073174-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1474  
ID ABO39338 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1475  
ID ABR75603 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1476  
ID ABR25527 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104541-A1.  
PD 05-JUN-2003.



Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1477  
ID ABM20037 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1478  
ID ABO46943 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1479  
ID ABO47248 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1480  
ID ADA83453 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1481  
ID ABR71679 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1482  
ID ABR72289 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1483  
ID ABR98628 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1484  
ID ABO06998 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1485  
ID ABR84951 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1486  
ID ABR73509 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054467-A1.

PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1487  
ID ABR76603 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1488  
ID ABR73204 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1489  
ID ABM18270 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1490  
ID ABO20729 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1491  
ID ABO25472 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1492  
ID ABO25777 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1493  
ID ABR94186 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1494  
ID ABR80093 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1495  
ID ABM11433 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1496



ID ABO33040 standard; protein; 649 AA.  
DE Human PRO polypeptide #192.  
PN US200306453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1497  
ID ABO30746 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1498  
ID ABO31051 standard; protein; 649 AA.  
DE Human secreted/transmembrane protein (PRO) #192.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1499  
ID ABM27357 standard; protein; 649 AA.  
DE Human secreted polypeptide PRO1865, SEQ ID NO:384.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 9.9%; Score 309; DB 6; Length 649;  
Query Match 22.3%; Pred. No. 4.8e-11;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;  
RESULT 1500  
ID AEF74347 standard; protein; 649 AA.  
DE Human PRO1865 protein SEQ ID NO:132.  
PN US2005260647-A1.  
PD 24-NOV-2005.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W L.  
Query Match 9.9%; Score 309; DB 10; Length 649;  
Best Local Similarity 22.3%; Pred. No. 4.8e-11;



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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 27, 2006, 12:10:19 ; Search time 50 Seconds  
(without alignments)  
1046.866 Million cell updates/sec

**Title:** US-10-677-669-69

Perfect score: 3135

Sequence: 1 MCSRVP LLLP LLL LALGPG.....PLMGFP GGLQ SPLHAKPYI 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%  
Maximum Match 100%

Maximum Match 100%  
Listing first 1500 summaries

Database : Issued Patents AA:\*

1: /EMC Celerra\_SIPS3/ptodata/2/iaa/5 COMB.per:\*

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2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
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3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:

4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pcp: \*

5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/pCTUS COMB. pep: \*

6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.ppe:\*

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7: /EMC_Celerra_SIDS3/pdata/2/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	3135	100.0	598	2	US-09-866-028-69	Sequence 69, Appl
2	3135	100.0	598	2	US-09-944-457-69	Sequence 69, Appl
3	3135	100.0	598	2	US-09-945-584-69	Sequence 69, Appl
4	3135	100.0	598	2	US-09-944-944-69	Sequence 69, Appl
5	3135	100.0	598	2	US-09-945-587-69	Sequence 69, Appl
6	3135	100.0	598	3	US-09-944-884-69	Sequence 69, Appl
7	3083.5	98.4	673	2	US-09-063-950-2	Sequence 2, Appl
8	3083.5	98.4	673	2	US-09-991-181-52	Sequence 52, Appl
9	3083.5	98.4	673	2	US-09-990-443-52	Sequence 52, Appl
10	3083.5	98.4	673	2	US-09-997-333-52	Sequence 52, Appl
11	3083.5	98.4	673	2	US-09-992-598-52	Sequence 52, Appl
12	3083.5	98.4	673	2	US-09-989-735-52	Sequence 52, Appl
13	3083.5	98.4	673	3	US-09-989-726-52	Sequence 52, Appl
14	3083.5	98.4	673	3	US-09-997-514-52	Sequence 52, Appl
15	3083.5	98.4	673	3	US-09-989-728-52	Sequence 52, Appl
16	3083.5	98.4	673	3	US-09-997-349-52	Sequence 52, Appl
17	3083.5	98.4	673	3	US-09-997-653-52	Sequence 52, Appl
18	3083.5	98.4	673	3	US-09-989-293A-52	Sequence 52, Appl
19	337	10.7	653	2	US-09-520-781-10	Sequence 10, Appl
20	337	10.7	653	2	US-09-957-187-10	Sequence 10, Appl
21	337	10.7	653	2	US-09-991-053-10	Sequence 10, Appl
22	333	10.6	590	2	US-09-520-781-12	Sequence 12, Appl
23	333	10.6	590	2	US-09-957-187-12	Sequence 12, Appl
24	333	10.6	590	2	US-09-991-053-12	Sequence 12, Appl
25	330	10.5	653	2	US-09-991-181-229	Sequence 229, Appl
26	330	10.5	653	2	US-09-990-444-229	Sequence 229, Appl



100	292.5	9.3	640	2	US-09-989-735-501	Sequence 501, App	173	252	8.0	566	2	US-09-775-803-12	Sequence 12, Appl
101	292.5	9.3	640	2	US-09-906-679A-292	Sequence 292, App	174	252	8.0	567	2	US-10-037-417-105	Sequence 105, App
102	292.5	9.3	640	3	US-09-988-726-501	Sequence 501, App	175	251	8.0	622	2	US-10-188-495-48	Sequence 48, Appl
103	292.5	9.3	640	3	US-09-997-514-501	Sequence 501, App	176	249.5	8.0	789	2	US-09-831-846-2	Sequence 2, Appl
104	292.5	9.3	640	3	US-09-989-728-501	Sequence 501, App	177	248	7.9	481	2	US-09-853-753-2	Sequence 2, Appl
105	292.5	9.3	640	3	US-09-907-841-232	Sequence 292, App	178	248	7.9	485	2	US-09-949-016-8704	Sequence 8704, Ap
106	292.5	9.3	640	3	US-09-997-349-501	Sequence 501, App	179	247.5	7.9	1525	2	US-09-191-647-2	Sequence 2, Appl
107	292.5	9.3	640	3	US-09-997-653-501	Sequence 501, App	180	247.5	7.9	1525	2	US-09-540-245A-2	Sequence 2, Appl
108	292.5	9.3	640	3	US-09-988-233A-501	Sequence 501, App	181	247.5	7.9	1525	2	US-09-540-153-2	Sequence 2, Appl
109	287.5	9.2	713	2	US-09-907-794A-245	Sequence 245, App	182	247.5	7.9	1525	2	US-10-289-776-2	Sequence 2, Appl
110	287.5	9.2	713	2	US-09-905-125A-245	Sequence 245, App	183	247.5	7.9	1529	2	US-10-188-495-67	Sequence 67, Appl
111	287.5	9.2	713	2	US-09-902-775A-245	Sequence 245, App	184	246.5	7.9	1529	2	US-09-312-283C-396	Sequence 396, App
112	287.5	9.2	713	2	US-09-906-700-245	Sequence 245, App	185	244	7.8	708	2	US-09-131-648-2	Sequence 2, Appl
113	287.5	9.2	713	2	US-09-903-603A-245	Sequence 245, App	186	244	7.8	708	2	US-09-907-794A-69	Sequence 69, Appl
114	287.5	9.2	713	2	US-09-904-920A-245	Sequence 245, App	187	244	7.8	708	2	US-09-905-125A-69	Sequence 69, Appl
115	287.5	9.2	713	2	US-09-909-064-245	Sequence 245, App	188	244	7.8	708	2	US-09-902-775A-69	Sequence 69, Appl
116	287.5	9.2	713	2	US-09-906-618-245	Sequence 245, App	189	244	7.8	708	2	US-09-906-700-69	Sequence 69, Appl
117	287.5	9.2	713	2	US-09-906-646-245	Sequence 245, App	190	244	7.8	708	2	US-09-903-603A-69	Sequence 69, Appl
118	287.5	9.2	713	2	US-09-904-462-245	Sequence 245, App	191	244	7.8	708	2	US-09-904-920A-69	Sequence 69, Appl
119	287.5	9.2	713	2	US-09-906-722A-245	Sequence 245, App	192	244	7.8	708	2	US-09-909-064-69	Sequence 69, Appl
120	287.5	9.2	713	2	US-09-905-449-245	Sequence 245, App	193	244	7.8	708	2	US-09-905-381A-69	Sequence 69, Appl
121	287.5	9.2	713	2	US-09-906-679A-245	Sequence 245, App	194	244	7.8	708	2	US-09-906-618-69	Sequence 69, Appl
122	287.5	9.2	713	2	US-09-907-841-245	Sequence 245, App	195	244	7.8	708	2	US-09-906-646-69	Sequence 69, Appl
123	287.5	9.2	713	2	US-10-104-047-2955	Sequence 2955, Ap	196	244	7.8	708	2	US-09-904-462-69	Sequence 69, Appl
124	287.5	9.2	713	3	US-09-907-841-245	Sequence 2960, Ap	197	244	7.8	708	2	US-09-902-736A-69	Sequence 69, Appl
125	287.5	9.2	713	2	US-10-104-047-2955	Sequence 50, Appl	198	244	7.8	708	2	US-09-906-722A-69	Sequence 69, Appl
126	284.5	9.1	745	2	US-08-190-802A-50	Sequence 50, Appl	199	244	7.8	708	2	US-09-905-449-69	Sequence 69, Appl
127	282.5	9.0	603	1	US-08-477-346-50	Sequence 50, Appl	200	244	7.8	708	2	US-09-903-562B-69	Sequence 69, Appl
128	281.5	9.0	603	2	US-08-473-089-50	Sequence 50, Appl	201	244	7.8	708	3	US-09-906-679A-69	Sequence 69, Appl
129	281.5	9.0	603	2	US-08-473-089-50	Sequence 50, Appl	202	244	7.8	708	3	US-09-907-841-69	Sequence 69, Appl
130	281.5	9.0	603	2	US-08-487-072A-50	Sequence 5, Appl	203	243.5	7.8	312	2	US-10-037-417-108	Sequence 108, App
131	281.5	9.0	603	2	US-08-386-485-6	Sequence 98, Appl	204	242.5	7.7	545	3	US-10-114-270-40	Sequence 40, Appl
132	271.5	8.7	353	2	US-10-037-417-98	Sequence 88, Appl	205	242.5	7.7	545	3	US-10-114-270-40	Sequence 40, Appl
133	271.5	8.7	1504	2	US-09-949-016-8448	Sequence 8448, Ap	206	241	7.7	380	2	US-09-461-325-161	Sequence 161, App
134	271	8.6	473	2	US-09-959-833A-400	Sequence 400, App	207	241	7.7	380	2	US-10-012-542-161	Sequence 161, App
135	271	8.6	473	2	US-10-020-445A-400	Sequence 400, App	208	241	7.7	380	2	US-08-115-123-161	Sequence 2, Appl
136	271	8.6	473	2	US-09-978-189-400	Sequence 400, App	209	240	7.7	560	2	US-08-592-500-2	Sequence 2, Appl
137	271	8.6	473	2	US-10-017-085A-400	Sequence 400, App	210	240	7.7	560	2	US-08-195-006-2	Sequence 4, Appl
138	271	8.6	473	2	US-10-017-085A-400	Sequence 400, App	211	240	7.7	560	2	US-09-063-950-4	Sequence 4, Appl
139	271	8.6	473	3	US-10-145-129A-400	Sequence 400, App	212	240	7.7	560	2	US-09-775-803-14	Sequence 14, Appl
140	271	8.6	473	3	US-10-013-929A-400	Sequence 400, App	213	240	7.7	560	5	PCT-US94-07644A-2	Sequence 2, Appl
141	271	8.6	473	3	US-10-013-917A-400	Sequence 400, App	214	236.5	7.5	222	5	PCT-US91-09055-3	Sequence 3, Appl
142	259	8.3	610	1	US-07-821-717B-6	Sequence 6, Appl	215	236.5	7.5	231	2	US-08-986-485-7	Sequence 7, Appl
143	259	8.3	610	1	US-08-119-262B-6	Sequence 6, Appl	216	230.5	7.4	544	2	US-10-068-426-1	Sequence 14, Appl
144	259	8.3	610	1	US-08-135-929A-11	Sequence 11, Appl	217	227	7.2	568	2	US-09-673-245-14	Sequence 3, Appl
145	259	8.3	610	1	US-08-234-265A-11	Sequence 21, Appl	218	226.5	7.2	544	2	US-10-068-426-3	Sequence 95, Appl
146	258	8.2	1523	2	US-09-182-024A-2	Sequence 2, Appl	219	226.5	7.2	557	2	US-10-037-417-95	Sequence 9, Appl
147	258	8.2	1523	2	US-10-012-231A-198	Sequence 198, App	220	226.5	7.2	719	2	US-10-094-749-2001	Sequence 2001, Ap
148	258	8.2	1523	2	US-10-015-389A-198	Sequence 198, App	221	225.5	7.2	544	2	US-10-068-426-2	Sequence 2, Appl
149	258	8.2	1523	2	US-10-006-768A-198	Sequence 198, App	222	225	7.2	735	2	US-09-191-647-9	Sequence 9, Appl
150	258	8.2	1523	2	US-10-015-671A-198	Sequence 198, App	223	225	7.2	735	2	US-09-540-245A-9	Sequence 9, Appl
151	258	8.2	1523	2	US-10-015-393A-198	Sequence 198, App	224	225	7.2	735	2	US-09-540-153-9	Sequence 9, Appl
152	258	8.2	1523	2	US-10-011-833A-198	Sequence 198, App	225	225	7.2	735	2	US-10-289-776-9	Sequence 9, Appl
153	258	8.2	1523	2	US-10-006-041A-198	Sequence 198, App	226	222	7.1	536	2	US-09-538-092-992	Sequence 992, App
154	258	8.2	1523	2	US-10-012-064A-198	Sequence 198, App	227	222	7.1	196	5	PCT-US91-09055-5	Sequence 5, Appl
155	258	8.2	1523	2	US-10-015-392A-198	Sequence 198, App	228	222	7.1	498	2	US-10-188-495-51	Sequence 51, Appl
156	258	8.2	1523	3	US-10-011-795B-198	Sequence 198, App	229	222	7.1	591	2	US-10-188-495-50	Sequence 50, Appl
157	258	8.2	1523	3	US-10-015-386A-198	Sequence 198, App	230	221.5	7.1	557	2	US-10-037-417-94	Sequence 94, Appl
158	258	8.2	1523	3	US-10-012-121A-198	Sequence 198, App	231	220.5	7.0	841	2	US-09-935-430-657	Sequence 657, App
159	258	8.2	1523	3	US-10-006-485A-198	Sequence 198, App	232	220.5	7.0	841	2	US-09-964-956-2	Sequence 2, Appl
160	258	8.2	1523	3	US-10-006-746A-198	Sequence 198, App	233	218.5	7.0	359	2	US-09-949-016-9732	Sequence 9732, Ap
161	258	8.2	1523	3	US-10-012-752A-198	Sequence 198, App	234	217.5	6.9	562	2	US-09-673-245-7	Sequence 7, Appl
162	258	8.2	1523	3	US-10-017-253A-198	Sequence 198, App	235	217.5	6.9	837	2	US-09-984-956-5	Sequence 5, Appl
163	258	8.2	1523	3	US-10-015-715A-198	Sequence 198, App	236	214.5	6.8	255	2	US-09-984-956-5	Sequence 232, App
164	258	8.2	1523	3	US-10-007-236A-198	Sequence 198, App	237	212	6.8	531	2	US-10-068-426-6	Sequence 6, Appl
165	258	8.2	1523	3	US-10-007-236A-198	Sequence 198, App	238	211	6.7	513	2	US-10-012-231A-385	Sequence 385, App
166	255.5	8.1	1480	2	US-09-191-647-7	Sequence 7, Appl	239	211	6.7	513	2	US-10-015-389A-385	Sequence 385, App
167	255.5	8.1	1480	2	US-09-540-245A-7	Sequence 7, Appl	240	211	6.7	513	2	US-10-006-768A-385	Sequence 385, App
168	255.5	8.1	1480	2	US-09-540-153-7	Sequence 7, Appl	241	211	6.7	513	2	US-10-006-671A-385	Sequence 385, App
169	255.5	8.1	1480	2	US-09-182-024A-5	Sequence 5, Appl	242	211	6.7	513	2	US-10-015-393A-385	Sequence 385, App
170	255.5	8.1	1480	2	US-10-289-776-7	Sequence 7, Appl	243	211	6.7	513	2	US-10-011-833A-385	Sequence 385, App
171	255.5	8.1	1480	5	PCT-US91-09055-2	Sequence 2, Appl	244	211	6.7	513	2	US-10-006-041A-385	Sequence 385, App
172	253	8.1	567	2	US-10-037-417-106	Sequence 106, App	245	211	6.7	513	2	US-10-012-064A-385	Sequence 385, App



245	211	6.7	513	2	US-10-015-392A-385	Sequence 385, App	319	197.5	6.3	616	3	US-10-015-715A-24	Sequence 24, Appl
246	211	6.7	513	3	US-10-011-795B-385	Sequence 385, App	320	197.5	6.3	616	3	US-10-007-236A-24	Sequence 24, Appl
247	211	6.7	513	3	US-10-015-386A-385	Sequence 385, App	321	196.5	6.3	716	2	US-09-312-283C-183	Sequence 183, App
248	211	6.7	513	3	US-10-012-121A-385	Sequence 385, App	322	196.5	6.3	771	2	US-09-188-930-183	Sequence 183, App
249	211	6.7	513	3	US-10-006-485A-385	Sequence 385, App	323	195.5	6.2	553	2	US-10-037-417-28	Sequence 28, Appl
250	211	6.7	513	3	US-10-006-746A-385	Sequence 385, App	324	195	6.2	620	2	US-09-907-794A-73	Sequence 73, Appl
251	211	6.7	513	3	US-10-012-752A-385	Sequence 385, App	325	195	6.2	620	2	US-09-905-125A-73	Sequence 73, Appl
252	211	6.7	513	3	US-10-017-253A-385	Sequence 385, App	326	195	6.2	620	2	US-09-902-775A-73	Sequence 73, Appl
253	211	6.7	513	3	US-10-015-519A-385	Sequence 385, App	327	195	6.2	620	2	US-09-906-700-73	Sequence 73, Appl
254	211	6.7	513	3	US-10-015-715A-385	Sequence 385, App	328	195	6.2	620	2	US-09-903-603A-73	Sequence 73, Appl
255	211	6.7	513	3	US-10-007-236A-385	Sequence 385, App	329	195	6.2	620	2	US-09-904-920A-73	Sequence 73, Appl
256	211	6.7	513	3	US-10-068-426-5	Sequence 5, Appl	330	195	6.2	620	2	US-09-909-064-73	Sequence 73, Appl
257	211	6.7	531	2	US-08-658-136-5	Sequence 5, Appl	331	195	6.2	620	2	US-09-905-381A-73	Sequence 73, Appl
258	210.5	6.7	4302	2	US-09-052-463-8	Sequence 8, Appl	332	195	6.2	620	2	US-09-906-618-73	Sequence 73, Appl
259	210.5	6.7	4302	2	US-08-422-582-8	Sequence 8, Appl	333	195	6.2	620	2	US-09-906-646-73	Sequence 73, Appl
260	210.5	6.7	4302	2	US-09-052-262-8	Sequence 8, Appl	334	195	6.2	620	2	US-09-904-462-73	Sequence 73, Appl
261	210.5	6.7	4302	2	US-10-068-426-4	Sequence 4, Appl	335	195	6.2	620	2	US-09-902-736A-73	Sequence 73, Appl
262	210	6.7	531	2	US-10-012-231A-397	Sequence 397, App	336	195	6.2	620	2	US-09-905-443-73	Sequence 73, Appl
263	209	6.7	353	2	US-10-015-389A-397	Sequence 397, App	337	195	6.2	620	2	US-09-906-722A-73	Sequence 73, Appl
264	209	6.7	353	2	US-10-006-768A-397	Sequence 397, App	338	195	6.2	620	2	US-09-903-562B-73	Sequence 73, Appl
265	209	6.7	353	2	US-10-015-393A-397	Sequence 397, App	339	195	6.2	620	2	US-09-906-679A-73	Sequence 73, Appl
266	209	6.7	353	2	US-10-011-833A-397	Sequence 397, App	340	195	6.2	620	2	US-09-907-841-73	Sequence 73, Appl
267	209	6.7	353	2	US-10-006-041A-397	Sequence 397, App	341	195	6.2	742	2	US-10-104-047-2807	Sequence 2807, Ap
268	209	6.7	353	2	US-10-012-064A-397	Sequence 397, App	342	195	6.2	832	2	US-09-935-430-660	Sequence 660, App
269	209	6.7	353	2	US-10-015-392A-397	Sequence 397, App	343	195	6.2	853	2	US-09-964-956-30	Sequence 30, Appl
270	209	6.7	353	2	US-10-011-795B-397	Sequence 397, App	344	194.5	6.2	699	2	US-09-949-016-6073	Sequence 6073, Ap
271	209	6.7	353	2	US-10-015-386A-397	Sequence 397, App	345	194.5	6.2	720	2	US-09-949-016-9819	Sequence 9819, Ap
272	209	6.7	353	2	US-10-012-121A-397	Sequence 397, App	346	193.5	6.2	224	5	PCT-US91-09055-4	Sequence 4, Appl
273	209	6.7	353	2	US-10-015-519A-397	Sequence 397, App	347	193.5	6.2	542	2	US-10-037-417-97	Sequence 97, Appl
274	209	6.7	353	2	US-10-006-485A-397	Sequence 397, App	348	190	6.1	1059	2	US-09-907-794A-290	Sequence 290, App
275	209	6.7	353	2	US-10-006-746A-397	Sequence 397, App	349	190	6.1	1059	2	US-09-905-125A-290	Sequence 290, App
276	209	6.7	353	2	US-10-012-752A-397	Sequence 397, App	350	190	6.1	1059	2	US-09-902-775A-290	Sequence 290, App
277	209	6.7	353	2	US-10-017-253A-397	Sequence 397, App	351	190	6.1	1059	2	US-09-906-700-290	Sequence 290, App
278	209	6.7	353	2	US-10-015-715A-397	Sequence 397, App	352	190	6.1	1059	2	US-09-903-603A-290	Sequence 290, App
279	209	6.7	353	2	US-10-007-236A-397	Sequence 397, App	353	190	6.1	1059	2	US-09-904-920A-290	Sequence 290, App
280	209	6.7	353	2	US-08-986-485-5	Sequence 5, Appl	354	190	6.1	1059	2	US-09-909-064-290	Sequence 290, App
281	209	6.7	1091	2	US-09-949-016-6625	Sequence 6625, Ap	355	190	6.1	1059	2	US-09-903-562B-290	Sequence 290, App
282	209	6.7	424	2	US-09-949-016-7950	Sequence 7950, Ap	356	190	6.1	1059	2	US-09-906-618-290	Sequence 290, App
283	208.5	6.6	415	2	US-09-935-430-659	Sequence 29, Appl	357	190	6.1	1059	2	US-09-906-646-290	Sequence 290, App
284	207.5	6.6	440	2	US-09-964-956-29	Sequence 29, Appl	358	190	6.1	1059	2	US-09-904-462-290	Sequence 290, App
285	207.5	6.6	440	2	US-09-935-430-658	Sequence 658, App	359	190	6.1	1059	2	US-09-902-736A-290	Sequence 290, App
286	207.5	6.6	798	2	US-09-964-956-28	Sequence 28, Appl	360	190	6.1	1059	2	US-09-906-722A-290	Sequence 290, App
287	207.5	6.6	798	2	US-08-986-485-2	Sequence 2, Appl	361	190	6.1	1059	2	US-09-903-562B-290	Sequence 290, App
288	206.5	6.6	1101	2	US-08-986-485-2	Sequence 2, Appl	362	190	6.1	1059	2	US-09-906-679A-290	Sequence 290, App
289	206	6.6	428	2	US-09-949-016-6625	Sequence 6625, Ap	363	190	6.1	1059	3	US-09-907-841-290	Sequence 290, App
290	206	6.6	433	2	US-09-949-016-8521	Sequence 8521, Ap	364	190	6.1	1059	2	US-09-907-794A-294	Sequence 294, App
291	205	6.5	4339	2	US-09-052-469-6	Sequence 6, Appl	365	190	6.1	1119	2	US-09-905-125A-294	Sequence 294, App
292	205	6.5	4339	2	US-08-422-582-6	Sequence 6, Appl	366	190	6.1	1119	2	US-09-902-775A-294	Sequence 294, App
293	205	6.5	4339	2	US-09-052-262-6	Sequence 2, Appl	367	190	6.1	1119	2	US-09-906-700-294	Sequence 294, App
294	203.5	6.5	4303	1	US-08-460-751-2	Sequence 2, Appl	368	190	6.1	1119	2	US-09-903-603A-294	Sequence 294, App
295	203.5	6.5	4303	2	US-09-479-467A-2	Sequence 2, Appl	369	190	6.1	1119	2	US-09-904-920A-294	Sequence 294, App
296	203.5	6.5	4303	2	US-09-655-160-2	Sequence 2513, Ap	370	190	6.1	1119	2	US-09-909-064-294	Sequence 294, App
297	201.5	6.4	606	2	US-10-094-749-2313	Sequence 105, App	371	190	6.1	1119	2	US-09-909-064-294	Sequence 294, App
298	200.5	6.4	302	2	US-09-482-273-105	Sequence 224A, Ap	372	190	6.1	1119	2	US-09-903-381A-294	Sequence 294, App
299	200.5	6.4	724	2	US-10-104-047-2224	Sequence 2504, Ap	373	190	6.1	1119	2	US-09-906-618-294	Sequence 294, App
300	199	6.3	321	2	US-10-104-047-2504	Sequence 2, Appl	374	190	6.1	1119	2	US-09-906-646-294	Sequence 294, App
301	198.5	6.3	1338	2	US-09-631-603-2	Sequence 24, Appl	375	190	6.1	1119	2	US-09-904-462-294	Sequence 294, App
302	197.5	6.3	616	2	US-10-012-231A-24	Sequence 24, Appl	376	190	6.1	1119	2	US-09-902-736A-294	Sequence 294, App
303	197.5	6.3	616	2	US-10-015-389A-24	Sequence 24, Appl	377	190	6.1	1119	2	US-09-906-722A-294	Sequence 294, App
304	197.5	6.3	616	2	US-10-006-768A-24	Sequence 24, Appl	378	190	6.1	1119	2	US-09-905-449-294	Sequence 294, App
305	197.5	6.3	616	2	US-10-015-671A-24	Sequence 24, Appl	379	190	6.1	1119	2	US-09-903-562B-294	Sequence 294, App
306	197.5	6.3	616	2	US-10-015-393A-24	Sequence 24, Appl	380	190	6.1	1119	2	US-09-906-679A-294	Sequence 294, App
307	197.5	6.3	616	2	US-10-011-833A-24	Sequence 24, Appl	381	190	6.1	1119	3	US-09-907-841-294	Sequence 294, App
308	197.5	6.3	616	2	US-10-006-041A-24	Sequence 24, Appl	382	189.5	6.0	301	2	US-10-068-426-9	Sequence 9, Appl
309	197.5	6.3	616	2	US-10-013-064A-24	Sequence 24, Appl	383	186.5	5.9	196	5	PCT-US91-09055-6	Sequence 6, Appl
310	197.5	6.3	616	2	US-10-015-392A-24	Sequence 24, Appl	384	186.5	5.9	799	3	US-09-396-985B-4	Sequence 4, Appl
311	197.5	6.3	616	3	US-10-011-795B-24	Sequence 24, Appl	385	186.5	5.9	839	3	US-09-396-985B-2	Sequence 2, Appl
312	197.5	6.3	616	3	US-10-015-386A-24	Sequence 24, Appl	386	186.5	5.9	839	3	US-09-396-985B-38	Sequence 98, Appl
313	197.5	6.3	616	3	US-10-012-121A-24	Sequence 24, Appl	387	186.5	5.9	844	2	US-09-949-016-9438	Sequence 9438, Ap
314	197.5	6.3	616	3	US-10-006-485A-24	Sequence 24, Appl	388	186	5.9	440	2	US-09-538-092-999	Sequence 999, App
315	197.5	6.3	616	3	US-10-006-746A-24	Sequence 24, Appl	389	186	5.9	451	2	US-09-949-016-9282	Sequence 9282, Ap
316	197.5	6.3	616	3	US-10-012-752A-24	Sequence 24, Appl	390	184	5.9	302	2	US-10-068-426-7	Sequence 7, Appl
317	197.5	6.3	616	3	US-10-017-253A-24	Sequence 24, Appl	391	184	5.9	320	1	US-07-613-083B-1	Sequence 1, Appl
318	197.5	6.3	616	3	US-10-015-519A-24	Sequence 24, Appl	392	184	5.9	320	1	US-07-613-083B-1	Sequence 1, Appl



392	184	5.9	368	2	US-09-949-016-6115	Sequence 6115, Ap	465	166	5.3	835	3	US-09-396-985B-6	Sequence 6, Appli
393	184	5.9	382	2	US-09-715-836A-9	Sequence 9, Appli	466	166	5.3	1112	2	US-09-353-585-2	Sequence 2, Appli
394	184	5.9	382	2	US-09-949-016-10542	Sequence 10542, A	467	164.5	5.2	501	2	US-09-907-794A-185	Sequence 185, App
395	183	5.8	662	2	US-09-538-092-1325	Sequence 1325, Ap	468	164.5	5.2	501	2	US-09-905-125A-185	Sequence 185, App
396	183	5.8	662	2	US-09-949-016-6619	Sequence 6619, Ap	469	164.5	5.2	501	2	US-09-902-775A-185	Sequence 185, App
397	183	5.8	665	2	US-09-949-016-10710	Sequence 10710, A	470	164.5	5.2	501	2	US-09-906-700-185	Sequence 185, App
398	182.5	5.8	379	2	US-09-866-028-2	Sequence 2, Appli	471	164.5	5.2	501	2	US-09-903-603A-185	Sequence 185, App
399	182.5	5.8	379	2	US-09-944-457-2	Sequence 2, Appli	472	164.5	5.2	501	2	US-09-904-920A-185	Sequence 185, App
400	182.5	5.8	379	2	US-09-945-584-2	Sequence 2, Appli	473	164.5	5.2	501	2	US-09-909-064A-185	Sequence 185, App
401	182.5	5.8	379	2	US-09-944-584-2	Sequence 2, Appli	474	164.5	5.2	501	2	US-09-905-381A-185	Sequence 185, App
402	182.5	5.8	379	3	US-09-945-587-2	Sequence 2, Appli	475	164.5	5.2	501	2	US-09-906-618-185	Sequence 185, App
403	182.5	5.8	379	3	US-09-944-884-2	Sequence 2, Appli	476	164.5	5.2	501	2	US-09-906-646-185	Sequence 185, App
404	182.5	5.8	958	2	US-09-706-594-5	Sequence 5, Appli	477	164.5	5.2	501	2	US-09-904-462-185	Sequence 185, App
405	182.5	5.8	966	2	US-09-964-956-32	Sequence 32, Appl	478	164.5	5.2	501	2	US-09-902-736A-185	Sequence 185, App
406	182	5.8	378	2	US-09-689-486-62	Sequence 62, Appl	479	164.5	5.2	501	2	US-09-906-722A-185	Sequence 185, App
407	182	5.8	378	2	US-09-973-424A-62	Sequence 62, Appl	480	164.5	5.2	501	2	US-09-905-449-185	Sequence 185, App
408	180	5.7	493	2	US-10-037-417-30	Sequence 30, Appl	481	164.5	5.2	501	2	US-09-903-562B-185	Sequence 185, App
409	180	5.7	989	3	US-09-954-987B-171	Sequence 171, App	482	164.5	5.2	501	2	US-09-906-679A-185	Sequence 185, App
410	179.5	5.7	515	3	US-10-162-335-92	Sequence 92, Appl	483	164.5	5.2	501	3	US-09-907-841-185	Sequence 8, Appli
411	179	5.7	290	2	US-10-068-426-10	Sequence 10, Appl	484	164.5	5.2	582	2	US-09-081-149-8	Sequence 10752, A
412	179	5.7	290	2	US-10-068-426-11	Sequence 11, Appl	485	164.5	5.2	582	2	US-09-949-016-10752	Sequence 2918, Ap
413	179	5.7	290	2	US-10-068-426-12	Sequence 12, Appl	486	164.5	5.2	858	2	US-10-104-047-2918	Sequence 91, Appl
414	179	5.7	302	2	US-10-068-426-8	Sequence 8, Appli	487	164	5.2	696	2	US-09-907-794A-91	Sequence 91, Appl
415	178	5.7	368	1	US-08-303-238-3	Sequence 3, Appli	488	164	5.2	696	2	US-09-905-125A-91	Sequence 91, Appl
416	178	5.7	368	2	US-08-458-834-3	Sequence 3, Appli	489	164	5.2	696	2	US-09-902-775A-91	Sequence 91, Appl
417	178	5.7	522	2	US-09-991-181-278	Sequence 278, App	490	164	5.2	696	2	US-09-906-700-91	Sequence 91, Appl
418	178	5.7	522	2	US-09-990-444-278	Sequence 278, App	491	164	5.2	696	2	US-09-903-620A-91	Sequence 91, Appl
419	178	5.7	522	2	US-09-997-333-278	Sequence 278, App	492	164	5.2	696	2	US-09-904-920A-91	Sequence 91, Appl
420	178	5.7	522	2	US-09-992-598-278	Sequence 278, App	493	164	5.2	696	2	US-09-905-064-91	Sequence 91, Appl
421	178	5.7	522	2	US-09-989-735-278	Sequence 278, App	494	164	5.2	696	2	US-09-908-381A-91	Sequence 91, Appl
422	178	5.7	522	2	US-10-094-749-2669	Sequence 2689, Ap	495	164	5.2	696	2	US-09-906-618-91	Sequence 91, Appl
423	178	5.7	522	3	US-09-989-726-278	Sequence 278, App	496	164	5.2	696	2	US-09-906-646-91	Sequence 91, Appl
424	178	5.7	522	3	US-09-997-514-278	Sequence 278, App	497	164	5.2	696	2	US-09-904-462-91	Sequence 91, Appl
425	178	5.7	522	3	US-09-989-728-278	Sequence 278, App	498	164	5.2	696	2	US-09-902-736A-91	Sequence 91, Appl
426	178	5.7	522	3	US-09-997-349-278	Sequence 278, App	499	164	5.2	696	2	US-09-905-449-91	Sequence 91, Appl
427	178	5.7	522	3	US-09-997-653-278	Sequence 278, App	500	164	5.2	696	2	US-09-903-562B-91	Sequence 91, Appl
428	178	5.7	522	3	US-09-989-293A-278	Sequence 278, App	501	164	5.2	696	2	US-09-906-679A-91	Sequence 91, Appl
429	178	5.7	1049	2	US-09-999-833A-496	Sequence 496, App	502	164	5.2	696	3	US-09-907-841-91	Sequence 91, Appl
430	178	5.7	1049	2	US-09-954-987B-170	Sequence 496, App	503	164	5.2	696	3	US-09-949-002-352	Sequence 352, App
431	178	5.7	1049	2	US-10-020-445A-496	Sequence 496, App	504	164	5.2	904	2	US-09-949-002-483	Sequence 483, App
432	178	5.7	1049	2	US-09-978-189-496	Sequence 496, App	505	164	5.2	910	2	US-09-081-149-7	Sequence 7, Appli
433	178	5.7	1049	3	US-10-017-085A-496	Sequence 496, App	506	163	5.2	582	2	US-09-081-149-7	Sequence 13, Appli
434	178	5.7	1049	3	US-10-145-129A-496	Sequence 496, App	507	163	5.2	753	2	US-09-056-383-13	Sequence 2, Appli
435	178	5.7	1049	3	US-10-013-929A-496	Sequence 496, App	508	161	5.1	559	2	US-09-081-149-2	Sequence 911, App
436	178	5.7	1052	3	US-10-013-917A-496	Sequence 496, App	509	160	5.1	942	2	US-10-101-464A-911	Sequence 192, App
437	178	5.7	1052	3	US-09-949-016-11508	Sequence 11508, A	510	158.5	5.1	1032	2	US-09-954-987B-192	Sequence 41554, A
438	177.5	5.7	1052	2	US-09-954-987B-175	Sequence 175, App	511	158	5.0	257	2	US-09-270-767-41554	Sequence 6781, Ap
439	176.5	5.6	522	2	US-10-104-047-2664	Sequence 2664, Ap	512	158	5.0	352	2	US-09-949-016-6781	Sequence 7689, Ap
440	175	5.6	368	7	5340934-2	Patent No. 5340934	513	158	5.0	374	2	US-09-949-016-7689	Sequence 42, Appl
441	173.5	5.5	998	2	US-10-101-464A-914	Sequence 914, App	514	157.5	5.0	236	1	US-08-442-063A-42	Sequence 522, App
442	173.5	5.5	282	1	US-08-442-063A-45	Sequence 45, Appl	515	157.5	5.0	672	2	US-09-949-002-522	Sequence 522, App
443	172.5	5.5	307	1	US-08-442-063A-48	Sequence 48, Appl	516	157	5.0	796	2	US-10-104-047-2293	Sequence 2293, Ap
444	172.5	5.5	333	1	US-08-442-063A-27	Sequence 27, Appl	517	156.5	5.0	376	2	US-09-538-092-1276	Sequence 1276, Ap
445	172.5	5.5	338	2	US-09-689-486-63	Sequence 63, Appl	518	156	5.0	975	2	US-09-949-016-7595	Sequence 7595, Ap
446	172.5	5.5	338	2	US-09-973-424A-63	Sequence 2, Appli	519	155	4.9	1041	2	US-09-999-833A-498	Sequence 498, App
447	172.5	5.5	342	1	US-08-272-919-2	Sequence 2, Appli	520	155	4.9	1041	2	US-09-954-987B-184	Sequence 184, App
448	172.5	5.5	342	1	PCT-US95-08542-2	Sequence 2, Appli	521	155	4.9	1041	2	US-09-954-987B-186	Sequence 186, App
449	172.5	5.5	342	1	US-08-303-238-4	Sequence 4, Appli	522	155	4.9	1041	2	US-10-020-445A-498	Sequence 498, App
450	172.5	5.5	359	1	US-08-458-834-4	Sequence 4, Appli	523	155	4.9	1041	2	US-09-978-189-498	Sequence 498, App
451	172.5	5.5	359	2	US-09-538-092-868	Sequence 4, Appli	524	155	4.9	1041	3	US-10-017-085A-498	Sequence 498, App
452	172.5	5.5	359	2	US-09-949-016-6143	Sequence 6143, Ap	525	155	4.9	1041	3	US-10-145-129A-498	Sequence 498, App
453	172.5	5.5	360	2	US-09-949-016-7925	Sequence 7925, Ap	526	155	4.9	1041	3	US-10-013-929A-498	Sequence 498, App
454	172.5	5.5	1388	2	US-10-153-469A-10	Sequence 10, Appl	527	155	4.9	1059	2	US-09-954-987B-187	Sequence 187, App
455	172.5	5.5	1388	2	US-10-104-889-10	Sequence 10, Appl	528	155	4.9	377	2	US-09-949-016-7949	Sequence 7949, Ap
456	172.5	5.5	373	2	US-09-724-864-43	Sequence 43, Appl	529	154.5	4.9	1495	2	US-08-522-726B-1	Sequence 1, Appli
457	170.5	5.4	907	2	US-09-170-496D-264	Sequence 264, App	530	154.5	4.9	1495	2	US-09-337-384-1	Sequence 2, Appli
458	170	5.4	907	2	US-09-170-496D-278	Sequence 278, App	531	153.5	4.9	894	1	US-08-372-892-2	Sequence 34, Appl
459	170	5.4	907	2	5340934-4	Patent No. 5340934	532	153.5	4.9	894	1	US-08-445-640-34	Sequence 34, Appl
460	169.5	5.4	353	7	US-09-954-987B-172	Sequence 172, App	533	153.5	4.9	894	2	US-08-170-558-34	Sequence 34, Appl
461	168	5.4	1049	2	PCT-US95-10509-2	Sequence 2, Appli	534	153.5	4.9	894	2	US-08-447-314-34	Sequence 34, Appl
462	167	5.3	746	5	US-09-353-585-3	Sequence 3, Appli	535	153.5	4.9	894	2	US-08-445-461-34	Sequence 34, Appl
463	167	5.3	1112	2	US-09-353-585-3	Sequence 3, Appli	536	153.5	4.9	894	2	US-09-223-490-34	Sequence 34, Appl
464	166.5	5.3	224	2	US-09-482-273-174	Sequence 174, App	537	153.5	4.9	894	2		



538	153.5	4.9	894	3	US-10-646-760-34	Sequence 34, Appl	611	143	4.6	935	2	US-09-477-962-107	Sequence 107, App
539	153.5	4.9	1032	2	US-09-954-987B-6	Sequence 6, Appl	612	142.5	4.5	141	2	US-09-270-767-31706	Sequence 31706, A
540	153	4.9	679	2	US-09-252-991A-18857	Sequence 18857, A	613	142.5	4.5	141	2	US-09-270-767-46923	Sequence 46923, A
541	153	4.9	699	2	US-10-237-551-143	Sequence 143, App	614	142.5	4.5	805	2	US-09-103-429A-4	Sequence 4, Appl
542	153	4.9	699	2	US-10-237-551-254	Sequence 254, App	615	142.5	4.5	807	2	US-09-294-663-4	Sequence 4, Appl
543	153	4.9	1248	2	US-10-042-810-4	Sequence 2, Appl	616	142	4.5	326	2	US-09-689-486-64	Sequence 64, Appl
544	153	4.9	1278	2	US-10-042-810-4	Sequence 4, Appl	617	142	4.5	326	2	US-09-973-424A-64	Sequence 64, Appl
545	152.5	4.9	164	2	US-10-104-047-2127	Sequence 2127, Ap	618	142	4.5	363	2	US-10-188-495-6	Sequence 6, Appl
546	152	4.8	786	2	US-09-949-002-351	Sequence 351, App	619	142	4.5	363	2	US-10-188-495-6	Sequence 6, Appl
547	152	4.8	796	2	US-09-949-002-386	Sequence 386, App	620	142	4.5	435	2	US-10-101-464A-901	Sequence 901, App
548	152	4.8	802	2	US-09-949-002-386	Sequence 386, App	621	142	4.5	435	2	US-10-101-464A-901	Sequence 901, App
549	151.5	4.8	455	2	US-10-188-495-3	Sequence 3, Appl	622	142	4.5	661	2	US-10-037-417-107	Sequence 5, Appl
550	151.5	4.8	1964	2	US-09-467-997-1	Sequence 1, Appl	623	140.5	4.5	345	2	US-10-101-464A-802	Sequence 107, App
551	151	4.8	832	2	US-09-270-767-46234	Sequence 46234, A	624	140.5	4.5	376	1	US-08-303-238-1	Sequence 802, App
552	151	4.8	835	3	US-09-396-988B-99	Sequence 99, Appl	625	140.5	4.5	376	2	US-08-458-834-1	Sequence 1, Appl
553	151	4.8	835	3	US-09-396-988B-99	Sequence 99, Appl	626	140	4.5	283	2	US-09-949-016-7910	Sequence 1, Appl
554	150.5	4.8	695	1	US-08-487-886-2	Sequence 104, App	627	140	4.5	547	2	US-10-101-464A-928	Sequence 928, App
555	150.5	4.8	695	2	US-08-482-855-2	Sequence 2, Appl	628	139	4.4	5179	2	US-09-538-092-1258	Sequence 1258, App
556	150.5	4.8	695	2	US-08-474-986-2	Sequence 2, Appl	629	138.5	4.4	710	2	US-10-104-047-3402	Sequence 3402, App
557	150	4.8	259	2	US-09-907-794A-71	Sequence 71, Appl	630	138.5	4.4	811	2	US-09-991-181-57	Sequence 57, Appl
558	150	4.8	259	2	US-09-905-125A-71	Sequence 71, Appl	631	138.5	4.4	811	2	US-09-990-444-57	Sequence 57, Appl
559	150	4.8	259	2	US-09-902-775A-71	Sequence 71, Appl	632	138.5	4.4	811	2	US-09-997-333-57	Sequence 57, Appl
560	150	4.8	259	2	US-09-906-700-71	Sequence 71, Appl	633	138.5	4.4	811	2	US-09-992-598-57	Sequence 57, Appl
561	150	4.8	259	2	US-09-903-603A-71	Sequence 71, Appl	634	138.5	4.4	811	3	US-09-989-735-57	Sequence 57, Appl
562	150	4.8	259	2	US-09-904-920A-71	Sequence 71, Appl	635	138.5	4.4	811	3	US-09-989-726-57	Sequence 57, Appl
563	150	4.8	259	2	US-09-906-064-71	Sequence 71, Appl	636	138.5	4.4	811	3	US-09-997-514-57	Sequence 57, Appl
564	150	4.8	259	2	US-09-905-381A-71	Sequence 71, Appl	637	138.5	4.4	811	3	US-09-989-728-57	Sequence 57, Appl
565	150	4.8	259	2	US-09-906-618-71	Sequence 71, Appl	638	138.5	4.4	811	3	US-09-997-349-57	Sequence 57, Appl
566	150	4.8	259	2	US-09-906-646-71	Sequence 71, Appl	639	138.5	4.4	811	3	US-09-989-293A-57	Sequence 57, Appl
567	150	4.8	259	2	US-09-904-462-71	Sequence 71, Appl	640	138	4.4	323	2	US-09-949-016-7924	Sequence 7924, App
568	150	4.8	259	2	US-09-902-736A-71	Sequence 71, Appl	641	138	4.4	1003	2	US-10-094-749-2528	Sequence 2528, App
569	150	4.8	259	2	US-09-906-722A-71	Sequence 71, Appl	642	137.5	4.4	141	2	US-10-094-749-2528	Sequence 45511, A
570	150	4.8	259	2	US-09-905-449-71	Sequence 71, Appl	643	137.5	4.4	884	7	5208144-8	Patent No. 5208144
571	150	4.8	259	2	US-09-905-449-71	Sequence 71, Appl	644	137	4.4	4544	1	US-08-469-486-52	Sequence 52, Appl
572	150	4.8	259	2	US-09-906-679A-71	Sequence 71, Appl	645	137	4.4	4544	1	US-08-469-658-52	Sequence 52, Appl
573	150	4.8	259	3	US-09-907-841-71	Sequence 71, Appl	646	136.5	4.4	984	2	US-10-101-464A-919	Sequence 919, App
574	150	4.8	513	2	US-09-068-804-14	Sequence 14, Appl	647	136.5	4.4	2972	2	US-09-579-181-2	Sequence 2, Appl
575	149	4.8	503	2	US-10-037-417-104	Sequence 104, App	648	136.5	4.4	3118	2	US-10-104-047-3292	Sequence 1, Appl
576	149	4.8	1025	1	US-08-475-891A-4	Sequence 4, Appl	649	136	4.3	287	2	US-07-757-342D-6	Sequence 6, Appl
577	149	4.8	1025	1	US-08-567-375-4	Sequence 4, Appl	650	136	4.3	692	2	US-09-461-657B-6	Sequence 6, Appl
578	149	4.8	1025	1	US-08-587-680A-4	Sequence 4, Appl	651	136	4.3	692	2	US-09-461-657B-6	Sequence 6, Appl
579	149	4.8	1026	2	US-09-623-551-18	Sequence 18, Appl	652	135.5	4.3	536	2	US-09-252-991A-31124	Sequence 31124, A
580	149	4.8	1504	2	US-09-364-206-2	Sequence 2, Appl	653	135.5	4.3	743	2	US-09-771-161A-164	Sequence 164, App
581	149	4.8	1874	2	US-09-331-403-2	Sequence 2, Appl	654	135.5	4.3	743	2	US-09-771-161A-164	Sequence 164, App
582	148.5	4.7	375	1	US-08-458-834-2	Sequence 2, Appl	655	135	4.3	446	2	US-10-101-464A-733	Sequence 733, App
583	148.5	4.7	375	1	US-08-458-834-2	Sequence 2, Appl	656	135	4.3	538	2	US-09-616-289-43	Sequence 43, Appl
584	147.5	4.7	570	2	US-09-565-501A-104	Sequence 104, App	657	135	4.3	538	2	US-09-976-740-43	Sequence 43, Appl
585	147.5	4.7	570	2	US-09-639-206A-104	Sequence 104, App	658	135	4.3	538	2	US-10-094-749-2425	Sequence 2425, App
586	147.5	4.7	570	2	US-09-874-923-104	Sequence 104, App	659	135	4.3	723	2	US-09-434-408-2	Sequence 2, Appl
587	147.5	4.7	1728	2	US-09-949-002-532	Sequence 532, App	660	135	4.3	907	2	US-08-783-774-2	Sequence 2, Appl
588	147	4.7	177	2	US-09-270-767-32705	Sequence 32705, A	661	135	4.3	907	2	US-09-328-599A-1	Sequence 1, Appl
589	147	4.7	265	2	US-09-270-767-47922	Sequence 47922, A	662	135	4.3	907	5	PCT-US95-04611A-19	Sequence 19, Appl
590	147	4.7	265	2	US-09-270-767-47922	Sequence 47922, A	663	135	4.3	802	2	US-09-823-240A-2	Sequence 2, Appl
591	147	4.7	2414	1	US-08-227-536-2	Sequence 2, Appl	664	134.5	4.3	536	2	US-09-292-225-21	Sequence 21, Appl
592	147	4.7	2414	1	US-09-538-092-1289	Sequence 1289, Ap	665	134	4.3	550	2	US-09-616-289-47	Sequence 47, Appl
593	147	4.7	2414	5	PCT-US95-04682-2	Sequence 2, Appl	666	134	4.3	550	2	US-09-616-289-47	Sequence 47, Appl
594	146.5	4.7	325	2	US-10-104-047-3320	Sequence 3320, Ap	667	134	4.3	555	2	US-09-976-740-47	Sequence 15, Appl
595	146.5	4.7	344	2	US-10-104-047-3358	Sequence 3358, Ap	668	134	4.3	555	2	US-09-292-225-15	Sequence 15, Appl
596	146.5	4.7	1404	1	US-08-400-159-2	Sequence 2, Appl	669	134	4.3	555	2	US-09-292-225-18	Sequence 18, Appl
597	146.5	4.7	1404	2	US-08-611-729A-2	Sequence 2, Appl	670	133.5	4.3	1166	2	US-10-101-464A-900	Sequence 900, App
598	146.5	4.7	1404	2	US-09-195-524-2	Sequence 2, Appl	671	133	4.2	652	2	US-10-104-047-3364	Sequence 3364, App
599	146	4.7	788	2	US-09-103-429A-3	Sequence 3, Appl	672	133	4.2	4391	2	US-10-006-011A-2	Sequence 2, Appl
600	146	4.7	788	2	US-09-294-663-3	Sequence 3, Appl	673	132.5	4.2	390	2	US-08-460-576-2	Sequence 2, Appl
601	146	4.7	885	1	US-08-372-892-4	Sequence 4, Appl	674	132.5	4.2	463	1	US-08-162-402B-9	Sequence 9, Appl
602	146	4.7	885	1	US-09-919-497-52	Sequence 52, Appl	675	132.5	4.2	579	2	US-09-325-932A-185	Sequence 185, App
603	145.5	4.6	2142	2	US-09-538-092-1142	Sequence 1142, Ap	676	132.5	4.2	583	2	US-09-641-612-2	Sequence 2, Appl
604	145.5	4.6	2142	2	US-09-949-002-371	Sequence 371, App	677	132.5	4.2	2035	1	US-08-046-585-5	Sequence 5, Appl
605	145	4.6	353	2	US-09-949-016-7923	Sequence 7923, Ap	678	132.5	4.2	2035	1	US-08-393-703-5	Sequence 5, Appl
606	145	4.6	1032	2	US-09-954-987B-3	Sequence 3, Appl	679	132.5	4.2	2035	5	PCT-US93-11721-5	Sequence 5, Appl
607	144	4.6	661	1	US-08-514-014-4	Sequence 4, Appl	680	132.5	4.2	2045	2	US-09-949-016-10491	Sequence 10491, A
608	144	4.6	661	1	US-08-833-823-4	Sequence 4, Appl	681	132.5	4.2	3122	2	US-10-237-551-201	Sequence 201, App
609	143.5	4.6	1274	1	US-09-095-443-2	Sequence 2, Appl	682	132.5	4.2	3122	2	US-10-237-551-250	Sequence 250, App
610	143.5	4.6	1636	3	US-10-433-794-1	Sequence 1, Appl	683	132	4.2	287	2	US-09-893-737-110	Sequence 110, App



684	132	4.2	465	1	US-08-162-402B-8	Sequence 8, Appli	757	126.5	4.0	685	2	US-09-641-612-7	Sequence 7, Appli
685	132	4.2	705	2	US-10-101-464A-894	Sequence 894, App	758	126.5	4.0	685	3	US-10-241-476-25	Sequence 25, Appl
686	132	4.2	979	2	US-08-514-213A-2	Sequence 2, Appli	759	126.5	4.0	919	2	US-10-101-464A-642	Sequence 642, App
687	132	4.2	979	2	US-09-015-399-5	Sequence 5, Appli	760	126.5	4.0	999	1	US-08-473-553A-5	Sequence 5, Appli
688	132	4.2	1003	2	US-09-949-016-11260	Sequence 11260, A	761	126	4.0	143	2	US-09-893-737-190	Sequence 190, App
689	131.5	4.2	461	2	US-10-037-417-96	Sequence 96, Appl	762	126	4.0	152	2	US-09-270-767-33594	Sequence 33594, A
690	131.5	4.2	571	2	US-09-252-991A-30533	Sequence 30533, A	763	126	4.0	775	2	US-09-949-016-8799	Sequence 8799, Ap
691	131	4.2	180	2	US-08-986-485-8	Sequence 8, Appli	764	126	4.0	1485	2	US-09-762-569-4	Sequence 4, Appli
692	131	4.2	227	2	US-10-101-464A-666	Sequence 666, App	765	126	4.0	1821	2	US-09-949-016-5938	Sequence 5938, Ap
693	131	4.2	279	2	US-09-270-767-41558	Sequence 41558, A	766	125.5	4.0	258	2	US-10-012-231A-153	Sequence 153, App
694	131	4.2	407	2	US-09-270-767-46649	Sequence 46649, A	767	125.5	4.0	258	2	US-10-015-389A-153	Sequence 153, App
695	131	4.2	709	2	US-09-180-439-6	Sequence 6, Appli	768	125.5	4.0	258	2	US-10-006-768A-153	Sequence 153, App
696	131	4.2	947	2	US-09-228-986-73	Sequence 73, Appl	769	125.5	4.0	258	2	US-10-015-671A-153	Sequence 153, App
697	131	4.2	947	2	US-10-101-464A-73	Sequence 73, Appl	770	125.5	4.0	258	2	US-10-015-393A-153	Sequence 153, App
698	131	4.2	1062	2	US-09-902-540-16313	Sequence 16313, A	771	125.5	4.0	258	2	US-10-011-833A-153	Sequence 153, App
699	131	4.2	1196	2	US-08-881-706-2	Sequence 2, Appli	772	125.5	4.0	258	2	US-10-006-041A-153	Sequence 153, App
700	131	4.2	1196	2	US-09-823-394-2	Sequence 2, Appli	773	125.5	4.0	258	2	US-10-012-064A-153	Sequence 153, App
701	131	4.2	1938	2	US-09-949-016-6609	Sequence 6609, Ap	774	125.5	4.0	258	3	US-10-011-795B-153	Sequence 153, App
702	130.5	4.2	843	2	US-10-101-464A-893	Sequence 893, App	775	125.5	4.0	258	3	US-10-015-386A-153	Sequence 153, App
703	130.5	4.2	878	2	US-09-556-706B-2	Sequence 2, Appli	776	125.5	4.0	258	3	US-10-012-121A-153	Sequence 153, App
704	130.5	4.2	878	2	US-09-724-418A-2	Sequence 2, Appli	777	125.5	4.0	258	3	US-10-006-485A-153	Sequence 153, App
705	130.5	4.2	3729	1	US-08-804-227C-4	Sequence 4, Appli	778	125.5	4.0	258	3	US-10-006-746A-153	Sequence 153, App
706	130	4.1	619	2	US-10-037-417-34	Sequence 34, Appl	779	125.5	4.0	258	3	US-10-012-752A-153	Sequence 153, App
707	130	4.1	645	2	US-10-101-464A-920	Sequence 920, App	780	125.5	4.0	258	3	US-10-017-253A-153	Sequence 153, App
708	129.5	4.1	550	2	US-09-252-991A-21295	Sequence 21295, A	781	125.5	4.0	258	3	US-10-015-519A-153	Sequence 153, App
709	129.5	4.1	912	5	PCN-US95-03747-2	Sequence 2, Appli	782	125.5	4.0	258	3	US-10-007-236A-153	Sequence 153, App
710	129.5	4.1	1251	3	US-10-114-270-80	Sequence 80, Appl	783	125.5	4.0	258	3	US-08-985-335-3	Sequence 3, Appli
711	129	4.1	363	2	US-09-270-767-44030	Sequence 44030, A	784	125.5	4.0	440	2	US-09-410-372-3	Sequence 54, Appl
712	129	4.1	823	2	US-09-252-991A-23655	Sequence 23655, A	785	125.5	4.0	764	2	US-07-741-453A-54	Sequence 60, Appl
713	129	4.1	885	2	US-09-252-991A-26129	Sequence 26129, A	786	125.5	4.0	764	2	US-07-741-453A-60	Sequence 2, Appli
714	129	4.1	1133	2	US-10-101-464A-809	Sequence 809, App	787	125.5	4.0	1129	2	US-09-023-905A-2	Sequence 237, App
715	129	4.1	1940	1	US-08-644-271-30	Sequence 30, Appl	788	125.5	4.0	419	2	US-10-002-344A-237	Sequence 25918, A
716	129	4.1	1940	2	US-09-077-955-34	Sequence 34, Appl	789	125.5	4.0	957	2	US-09-252-991A-35918	Sequence 20408, A
717	129	4.1	1940	2	US-10-016-283-34	Sequence 34, Appl	790	125	4.0	1139	2	US-09-513-505-2	Sequence 2, Appli
718	129	4.1	2321	2	US-09-230-652-2	Sequence 2, Appli	791	125	4.0	2023	2	US-09-491-356C-8	Sequence 86, Appl
719	129	4.1	2321	2	US-09-612-226B-2	Sequence 2, Appli	792	125	4.0	2026	2	US-09-538-092-1377	Sequence 1377, Ap
720	128.5	4.1	188	1	US-08-836-854-15	Sequence 15, Appl	793	125	4.0	2124	2	US-09-538-092-1377	Sequence 17231, A
721	128.5	4.1	446	1	US-10-104-047-3233	Sequence 3233, Ap	794	125	4.0	2294	2	US-09-252-991A-17231	Sequence 61021, A
722	128.5	4.1	508	2	US-10-101-464A-953	Sequence 953, App	795	125	4.0	283	2	US-10-211-689-4	Sequence 4, Appli
723	128.5	4.1	854	2	US-10-101-464A-896	Sequence 896, App	796	125	4.0	298	2	US-09-232-160-17	Sequence 17, Appl
724	128.5	4.1	864	2	US-09-502-540-10416	Sequence 10416, A	797	124.5	4.0	298	2	US-09-800-729-87	Sequence 87, Appl
725	128.5	4.1	865	2	US-08-567-375-2	Sequence 2, Appli	798	124.5	4.0	298	2	US-09-800-729-121	Sequence 121, App
726	128.5	4.1	1023	1	US-08-567-375-2	Sequence 2, Appli	799	124.5	4.0	298	2	US-10-000-489-22	Sequence 22, Appl
727	128.5	4.1	1023	1	US-08-567-375-2	Sequence 2, Appli	800	124.5	4.0	298	2	US-09-832-129-50	Sequence 50, Appl
728	128.5	4.1	1023	1	US-08-567-375-2	Sequence 2, Appli	801	124.5	4.0	298	2	US-10-211-689-2	Sequence 2, Appli
729	128	4.1	475	2	US-09-252-991A-30242	Sequence 30242, A	802	124.5	4.0	298	2	US-09-992-095B-22	Sequence 22, Appl
730	128	4.1	538	1	US-08-541-759B-2	Sequence 2, Appli	803	124.5	4.0	307	2	US-10-000-986A-22	Sequence 9817, Ap
731	128	4.1	717	2	US-10-101-464A-810	Sequence 810, App	804	124.5	4.0	307	2	US-09-949-016-9817	Sequence 9818, A
732	127.5	4.1	1006	3	US-10-415-147-12	Sequence 12, Appl	805	124.5	4.0	307	2	US-09-949-016-9818	Sequence 250, App
733	127.5	4.1	1522	2	US-10-114-270-84	Sequence 84, Appl	806	124.5	4.0	307	2	US-09-907-794A-250	Sequence 250, App
734	127.5	4.1	1581	2	US-10-144-198-31	Sequence 31, Appl	807	124.5	4.0	546	2	US-09-905-125A-250	Sequence 250, App
735	127.5	4.1	1581	2	US-09-949-002-414	Sequence 414, App	808	124.5	4.0	546	2	US-09-902-775A-250	Sequence 250, App
736	127.5	4.1	3969	2	US-08-061-376-5	Sequence 5, Appli	809	124.5	4.0	546	2	US-09-906-700A-250	Sequence 250, App
737	127.5	4.1	3969	2	US-09-538-092-1262	Sequence 1262, Ap	810	124.5	4.0	546	2	US-09-903-603A-250	Sequence 250, App
738	127	4.1	2669	2	US-09-270-767-32658	Sequence 32658, A	811	124.5	4.0	546	2	US-09-904-920A-250	Sequence 250, App
739	127	4.1	615	2	US-09-252-991A-26695	Sequence 26695, A	812	124.5	4.0	546	2	US-09-909-064-250	Sequence 250, App
740	126.5	4.0	141	2	US-09-270-767-32244	Sequence 32244, A	813	124.5	4.0	546	2	US-09-905-381A-250	Sequence 250, App
741	126.5	4.0	141	2	US-09-270-767-47461	Sequence 47461, A	814	124.5	4.0	546	2	US-09-906-618-250	Sequence 250, App
742	126.5	4.0	438	2	US-09-991-181-129	Sequence 129, App	815	124.5	4.0	546	2	US-09-906-646-250	Sequence 250, App
743	126.5	4.0	438	2	US-09-990-444-129	Sequence 129, App	816	124.5	4.0	546	2	US-09-904-462-250	Sequence 250, App
744	126.5	4.0	438	2	US-09-997-333-129	Sequence 129, App	817	124.5	4.0	546	2	US-09-902-736A-250	Sequence 250, App
745	126.5	4.0	438	2	US-09-992-598-129	Sequence 129, App	818	124.5	4.0	546	2	US-09-906-722A-250	Sequence 250, App
746	126.5	4.0	438	2	US-09-989-735-129	Sequence 129, App	819	124.5	4.0	546	2	US-09-905-449-250	Sequence 250, App
747	126.5	4.0	438	3	US-09-989-726-129	Sequence 129, App	820	124.5	4.0	546	2	US-09-903-562B-250	Sequence 250, App
748	126.5	4.0	438	3	US-09-997-514-129	Sequence 129, App	821	124.5	4.0	546	2	US-09-906-679A-250	Sequence 250, App
749	126.5	4.0	438	3	US-09-989-728-129	Sequence 129, App	822	124.5	4.0	546	2	US-09-907-841-250	Sequence 250, App
750	126.5	4.0	438	3	US-09-997-349-129	Sequence 129, App	823	124.5	4.0	546	2	US-09-906-722A-250	Sequence 250, App
751	126.5	4.0	438	3	US-09-997-653-129	Sequence 129, App	824	124.5	4.0	546	2	US-09-905-449-250	Sequence 250, App
752	126.5	4.0	659	2	US-09-989-293A-129	Sequence 3, Appli	825	124.5	4.0	546	2	US-09-906-679A-250	Sequence 250, App
753	126.5	4.0	659	2	US-08-423-753-3	Sequence 3, Appli	826	124.5	4.0	623	3	US-09-907-841-250	Sequence 6530, Ap
754	126.5	4.0	659	3	US-10-241-476-3	Sequence 2, Appli	827	124.5	4.0	998	2	US-09-949-016-8799	Sequence 8799, Ap
755	126.5	4.0	685	2	US-08-872-855-2	Sequence 25, Appli	828	124.5	4.0	1042	2	US-10-101-464A-895	Sequence 895, App
756	126.5	4.0	685	2	US-09-423-753-25	Sequence 25, Appli	829	124.5	4.0	1042	2	US-09-252-991A-30444	Sequence 30444, A



830	124.5	4.0	1709	2	US-09-949-016-10503	Sequence 10503, A	903	120.5	3.8	141	1	US-08-442-063A-36	Sequence 36, Appl
831	124	4.0	277	2	US-07-741-453A-58	Sequence 58, Appl	904	120.5	3.8	426	2	US-09-252-991A-24450	Sequence 24450, A
832	124	4.0	707	2	US-09-228-986-80	Sequence 80, Appl	905	120.5	3.8	464	2	US-09-716-964B-4	Sequence 4, Appl
833	124	4.0	707	2	US-10-101-464A-80	Sequence 80, Appl	906	120.5	3.8	562	2	US-09-902-540-13269	Sequence 13269, A
834	124	4.0	1457	2	US-08-665-259-27	Sequence 27, Appl	907	120.5	3.8	787	2	US-09-721-383-2	Sequence 2, Appl
835	124	4.0	1457	2	US-08-762-500-27	Sequence 27, Appl	908	120.5	3.8	787	2	US-09-721-137-2	Sequence 2, Appl
836	124	4.0	1472	2	US-09-032-438C-119	Sequence 119, Appl	909	120.5	3.8	787	2	US-09-721-251-2	Sequence 2, Appl
837	123.5	3.9	1312	2	US-09-041-886-19	Sequence 19, Appl	910	120.5	3.8	787	2	US-10-114-764-2	Sequence 2, Appl
838	123.5	3.9	1312	2	US-09-648-281-2	Sequence 19, Appl	911	120.5	3.8	998	2	US-10-101-464A-931	Sequence 931, Appl
839	123.5	3.9	1312	2	US-09-707-919A-19	Sequence 19, Appl	912	120.5	3.8	1104	2	US-09-981-953A-4	Sequence 4, Appl
840	123.5	3.9	1312	2	US-09-083-268-3	Sequence 3, Appl	913	120.5	3.8	1587	2	US-09-949-002-354	Sequence 354, Appl
841	123.5	3.9	1312	2	US-08-981-998A-3	Sequence 3, Appl	914	120.5	3.8	1610	2	US-09-548-473B-4	Sequence 4, Appl
842	123	3.9	526	2	US-10-101-464A-998	Sequence 998, Appl	915	120.5	3.8	1665	2	US-09-858-664A-2	Sequence 2, Appl
843	123	3.9	526	2	US-09-252-991A-23688	Sequence 23688, A	916	120.5	3.8	1665	2	US-10-274-978-2	Sequence 2, Appl
844	123	3.9	557	2	US-09-248-796A-26892	Sequence 26892, A	917	120.5	3.8	1665	2	US-10-697-263-2	Sequence 2, Appl
845	123	3.9	888	1	US-08-445-640-35	Sequence 35, Appl	918	120.5	3.8	2596	2	US-09-548-473B-6	Sequence 6, Appl
846	123	3.9	888	1	US-08-170-558-35	Sequence 35, Appl	919	120.5	3.8	2630	3	US-10-077-130-2	Sequence 2, Appl
847	123	3.9	888	2	US-08-447-314-35	Sequence 35, Appl	920	120.5	3.8	7968	3	US-10-077-130-5	Sequence 5, Appl
848	123	3.9	888	2	US-08-445-461-35	Sequence 35, Appl	921	120.5	3.8	130	2	US-09-270-767-33086	Sequence 33086, A
849	123	3.9	888	2	US-09-223-490-35	Sequence 35, Appl	922	120	3.8	130	2	US-09-270-767-48303	Sequence 48303, A
850	123	3.9	888	3	US-10-646-760-35	Sequence 35, Appl	923	120	3.8	467	2	US-09-046-736-2	Sequence 2, Appl
851	123	3.9	924	1	US-08-481-130-28	Sequence 28, Appl	924	120	3.8	523	1	US-08-473-553A-3	Sequence 3, Appl
852	123	3.9	924	1	US-08-656-984A-28	Sequence 28, Appl	925	120	3.8	569	2	US-09-514-245-22	Sequence 22, Appl
853	123	3.9	924	1	US-08-485-604-28	Sequence 28, Appl	926	120	3.8	603	2	US-09-906-779-4	Sequence 4, Appl
854	123	3.9	924	1	US-08-487-595-28	Sequence 28, Appl	927	120	3.8	696	2	US-09-758-759-125	Sequence 125, Appl
855	122.5	3.9	335	3	US-10-114-270-34	Sequence 34, Appl	928	120	3.8	710	2	US-10-094-749-2315	Sequence 2315, Appl
856	122.5	3.9	335	3	US-10-114-270-36	Sequence 36, Appl	929	120	3.8	2556	2	US-08-899-232-2	Sequence 2, Appl
857	122.5	3.9	494	2	US-09-641-612-5	Sequence 5, Appl	930	120	3.8	2556	2	US-09-121-457-2	Sequence 2, Appl
858	122.5	3.9	585	2	US-09-252-991A-18875	Sequence 18875, A	931	120	3.8	520	2	US-09-107-433-3721	Sequence 3721, Appl
859	122.5	3.9	596	2	US-09-180-439-3	Sequence 3, Appl	932	119.5	3.8	608	2	US-09-949-016-11148	Sequence 11148, A
860	122.5	3.9	968	2	US-09-180-439-4	Sequence 4, Appl	933	119.5	3.8	608	2	US-09-949-016-11149	Sequence 11149, A
861	122.5	3.9	968	2	US-09-180-439-3	Sequence 3, Appl	934	119.5	3.8	608	2	US-09-949-016-11150	Sequence 11150, A
862	122.5	3.9	1016	2	US-09-180-439-8	Sequence 8, Appl	935	119.5	3.8	608	2	US-09-949-016-11151	Sequence 11151, A
863	122.5	3.9	1036	2	US-09-771-161A-255	Sequence 255, Appl	936	119.5	3.8	1034	2	US-09-252-991A-28921	Sequence 28921, A
864	122.5	3.9	1036	2	US-09-771-161A-256	Sequence 256, Appl	937	119.5	3.8	1048	2	US-09-171-699-10	Sequence 10, Appl
865	122	3.9	191	2	US-09-461-325-186	Sequence 186, Appl	938	119.5	3.8	1149	2	US-08-560-005-5	Sequence 5, Appl
866	122	3.9	191	2	US-10-012-542-186	Sequence 186, Appl	939	119.5	3.8	1149	2	US-09-418-540-5	Sequence 5, Appl
867	122	3.9	191	2	US-10-115-123-412	Sequence 412, Appl	940	119.5	3.8	1149	2	US-09-969-528-5	Sequence 5, Appl
868	122	3.9	206	2	US-09-461-325-412	Sequence 412, Appl	941	119.5	3.8	1345	3	US-10-433-794-17	Sequence 17, Appl
869	122	3.9	206	2	US-10-012-542-412	Sequence 412, Appl	942	119.5	3.8	1596	2	US-09-538-092-887	Sequence 887, Appl
870	122	3.9	206	2	US-10-115-123-412	Sequence 412, Appl	943	119.5	3.8	304	2	US-10-101-464A-717	Sequence 717, Appl
871	122	3.9	312	2	US-09-270-767-31750	Sequence 31750, A	944	119	3.8	319	2	US-08-630-172-12	Sequence 12, Appl
872	122	3.9	328	1	US-08-414-926A-9	Sequence 9, Appl	945	119	3.8	319	2	US-09-375-419-12	Sequence 12, Appl
873	122	3.9	328	1	US-08-928-922-9	Sequence 9, Appl	946	119	3.8	528	2	US-08-928-213B-8	Sequence 8, Appl
874	122	3.9	328	2	US-09-253-682-9	Sequence 9, Appl	947	119	3.8	593	2	US-09-252-991A-20441	Sequence 20441, A
875	122	3.9	328	2	US-09-527-657-9	Sequence 9, Appl	948	119	3.8	784	2	US-09-982-308B-23	Sequence 23, Appl
876	122	3.9	328	2	US-09-892-100-9	Sequence 9, Appl	949	119	3.8	1081	2	US-09-369-364A-17	Sequence 17, Appl
877	122	3.9	481	2	US-09-949-016-9748	Sequence 9748, Appl	950	119	3.8	171	2	US-09-270-767-43049	Sequence 43049, A
878	122	3.9	495	2	US-09-252-991A-31949	Sequence 31949, A	951	118.5	3.8	422	2	US-09-949-016-8251	Sequence 8251, Appl
879	122	3.9	515	2	US-09-252-991A-28127	Sequence 28127, A	952	118.5	3.8	430	2	US-09-949-016-8782	Sequence 8782, Appl
880	122	3.9	527	2	US-09-370-838-216	Sequence 216, Appl	953	118.5	3.8	486	1	US-08-450-360-2	Sequence 2, Appl
881	122	3.9	527	2	US-09-854-133-216	Sequence 216, Appl	954	118.5	3.8	883	2	US-10-188-495-72	Sequence 72, Appl
882	122	3.9	529	2	US-09-716-964B-2	Sequence 2, Appl	955	118.5	3.8	1166	2	US-10-104-047-2949	Sequence 2949, Appl
883	121.5	3.9	320	2	US-09-325-932A-190	Sequence 190, Appl	956	118.5	3.8	1321	1	US-08-317-310A-64	Sequence 64, Appl
884	121.5	3.9	344	2	US-10-094-749-2951	Sequence 2951, Appl	957	118.5	3.8	149	2	US-09-270-767-32618	Sequence 32618, A
885	121.5	3.9	477	2	US-09-252-991A-19831	Sequence 19831, A	958	118	3.8	149	2	US-09-270-767-47835	Sequence 47835, A
886	121.5	3.9	695	2	US-09-248-796A-18020	Sequence 18020, A	959	118	3.8	462	2	US-09-252-991A-20814	Sequence 20814, A
887	121.5	3.9	818	2	US-10-104-047-2546	Sequence 2546, Appl	960	118	3.8	947	2	US-09-252-991A-21335	Sequence 21335, A
888	121.5	3.9	1225	2	US-09-501-171-4	Sequence 4, Appl	961	118	3.8	1044	2	US-09-252-991A-18853	Sequence 18853, A
889	121.5	3.9	1225	2	US-09-949-016-6063	Sequence 6063, Appl	962	118	3.8	1064	2	US-09-252-991A-17508	Sequence 17508, A
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891	121.5	3.9	1252	1	US-08-199-780-3	Sequence 3, Appl	964	118	3.8	1864	1	US-10-071-900-3	Sequence 3, Appl
892	121.5	3.9	1252	1	US-08-316-650-3	Sequence 3, Appl	965	118	3.8	2471	1	US-08-804-227C-3	Sequence 3, Appl
893	121.5	3.9	1253	2	US-08-479-722B-4	Sequence 4, Appl	966	118	3.8	2471	1	US-08-185-432-16	Sequence 16, Appl
894	121.5	3.9	1253	2	US-09-592-685-4	Sequence 4, Appl	967	118	3.8	2471	1	US-08-803-590A-19	Sequence 19, Appl
895	121	3.9	499	2	US-09-049-672A-1	Sequence 1, Appl	968	118	3.8	2471	2	US-08-532-384-19	Sequence 19, Appl
896	121	3.9	739	2	US-09-902-540-10606	Sequence 10606, A	969	118	3.8	2471	2	US-08-899-232-1	Sequence 1, Appl
897	121	3.9	910	2	US-09-228-986-72	Sequence 72, Appl	970	118	3.8	129	2	US-09-121-457-1	Sequence 1, Appl
898	121	3.9	910	2	US-10-101-464A-72	Sequence 72, Appl	971	118	3.8	189	2	US-09-513-999C-4304	Sequence 4304, Appl
899	121	3.9	955	2	US-10-094-749-2652	Sequence 2652, Appl	972	117.5	3.7	190	2	US-10-101-464A-517	Sequence 517, Appl
900	121	3.9	1139	2	US-09-513-505-4	Sequence 4, Appl	973	117.5	3.7	190	1	US-08-441-629-4	Sequence 4, Appl
901	121	3.9	1742	3	US-09-958-359-23	Sequence 23, Appl	974	117.5	3.7	190	2	US-08-776-207-4	Sequence 4, Appl
902	120.5	3.8	54	2	US-09-973-424A-71	Sequence 71, Appl	975	117.5	3.7	190	2		



976	117.5	3.7	190	2	US-09-507-773-4	Sequence 4, Appli	1049	115.5	3.7	1093	5	PCT-US94-04496-55	Sequence 55, Appli
977	117.5	3.7	190	2	US-10-036-447-4	Sequence 4, Appli	1050	115	3.7	305	2	US-09-325-932A-188	Sequence 188, App
978	117.5	3.7	190	5	PCT-US95-09172-4	Sequence 4, Appli	1051	115	3.7	447	1	US-08-450-360-4	Sequence 4, Appli
979	117.5	3.7	190	2	US-10-101-464A-730	Sequence 730, App	1052	115	3.7	717	2	US-10-094-749-2120	Sequence 2120, Ap
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981	117.5	3.7	563	1	US-08-484-101B-36	Sequence 36, Appl	1054	115	3.7	764	2	US-07-741-453A-61	Sequence 61, Appl
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983	117.5	3.7	635	1	US-08-714-524D-36	Sequence 36, Appl	1056	115	3.7	984	2	US-09-287-354-2	Sequence 2, Appli
984	117.5	3.7	635	2	US-08-714-524D-50	Sequence 50, Appl	1057	115	3.7	984	2	US-10-024-368-6	Sequence 6, Appli
985	117.5	3.7	635	2	US-10-101-464A-889	Sequence 889, App	1058	115	3.7	1053	2	US-09-513-505-6	Sequence 21827, A
986	117.5	3.7	996	2	US-10-101-464A-933	Sequence 933, App	1059	115	3.7	1093	2	US-09-252-991A-21827	Sequence 4, Appli
987	117.5	3.7	1118	2	US-09-252-991A-24340	Sequence 24340, A	1060	115	3.7	1189	2	US-09-287-354-4	Sequence 6931, Ap
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989	117.5	3.7	1706	1	US-08-459-588-2	Sequence 2, Appli	1062	115	3.7	1189	2	US-08-882-046-5	Sequence 5, Appli
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991	117.5	3.7	1706	2	US-08-516-859A-2	Sequence 2, Appli	1064	115	3.7	1219	2	US-09-949-002-398	Sequence 398, App
992	117.5	3.7	1706	2	US-09-586-472-2	Sequence 2, Appli	1065	114.5	3.7	2415	2	US-09-949-002-398	Sequence 398, App
993	117.5	3.7	1706	2	US-09-528-706-2	Sequence 2, Appli	1066	114.5	3.7	166	2	US-09-270-767-59438	Sequence 59438, A
994	117.5	3.7	1706	2	US-10-024-450-2	Sequence 2, Appli	1067	114.5	3.7	545	2	US-09-949-002-297	Sequence 297, App
995	117.5	3.7	1706	2	US-10-142-650-3	Sequence 3, Appli	1068	114.5	3.7	545	2	US-09-509-595B-8	Sequence 8, Appli
996	117	3.7	401	2	US-09-252-991A-32529	Sequence 32529, A	1069	114.5	3.7	545	2	US-09-509-595B-8	Sequence 8, Appli
997	117	3.7	655	1	US-08-148-910-12	Sequence 12, Appl	1070	114.5	3.7	587	2	US-09-949-016-8709	Sequence 8709, Ap
998	117	3.7	655	1	US-08-448-937A-12	Sequence 12, Appl	1071	114.5	3.7	587	2	US-09-949-016-8709	Sequence 8709, Ap
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1001	117	3.7	980	1	US-08-473-553A-6	Sequence 6, Appli	1074	114.5	3.7	935	2	US-10-101-464A-890	Sequence 890, App
1002	117	3.7	985	2	US-08-473-553A-2	Sequence 2, Appli	1075	114.5	3.7	1010	2	US-09-902-540-16200	Sequence 16200, A
1003	117	3.7	1055	2	US-09-214-278-2	Sequence 2, Appli	1076	114.5	3.7	1010	2	US-08-882-046-7	Sequence 7, Appli
1004	117	3.7	1055	2	US-09-855-722-2	Sequence 2, Appli	1077	114.5	3.7	1017	2	US-09-566-047-7	Sequence 7, Appli
1005	117	3.7	1148	2	US-08-882-046-4	Sequence 4, Appli	1078	114.5	3.7	1017	2	US-09-600-776-6	Sequence 6, Appli
1006	117	3.7	1148	2	US-09-566-047-4	Sequence 4, Appli	1079	114.5	3.7	1017	2	US-09-965-830-6	Sequence 6, Appli
1007	117	3.7	1193	1	US-08-400-159-10	Sequence 10, Appl	1080	114.5	3.7	1036	2	US-09-068-740A-6	Sequence 6, Appli
1008	117	3.7	1193	2	US-08-611-729A-10	Sequence 10, Appl	1081	114.5	3.7	1067	2	US-09-573-536C-18	Sequence 18, Appl
1009	117	3.7	1193	2	US-09-310-685-8	Sequence 8, Appli	1082	114.5	3.7	1162	2	US-09-573-536C-18	Sequence 2, Appli
1010	117	3.7	1193	2	US-09-310-685-8	Sequence 8, Appli	1083	114.5	3.7	1162	2	US-08-728-333A-2	Sequence 2, Appli
1011	117	3.7	1212	2	US-09-214-278-3	Sequence 3, Appli	1084	114.5	3.7	1162	2	US-09-410-399-2	Sequence 2, Appli
1012	117	3.7	1212	2	US-09-855-722-3	Sequence 3, Appli	1085	114.5	3.7	1162	2	US-09-894-273-2	Sequence 2, Appli
1013	117	3.7	1238	2	US-09-214-278-5	Sequence 5, Appli	1086	114.5	3.7	1187	2	US-09-068-740A-7	Sequence 7, Appli
1014	117	3.7	1238	2	US-09-214-278-5	Sequence 5, Appli	1087	114.5	3.7	1208	2	US-09-199-865-1	Sequence 1, Appli
1015	117	3.7	1257	2	US-09-855-722-5	Sequence 5, Appli	1088	114.5	3.7	1208	2	US-09-199-865-1	Sequence 1, Appli
1016	117	3.7	1257	2	US-08-611-729A-8	Sequence 8, Appli	1089	114.5	3.7	1218	2	US-08-400-159-6	Sequence 6, Appli
1017	117	3.7	1257	2	US-09-195-524-8	Sequence 8, Appli	1090	114.5	3.7	1218	2	US-08-611-729A-6	Sequence 6, Appli
1018	117	3.7	2038	3	US-09-310-685-6	Sequence 6, Appli	1091	114.5	3.7	1218	2	US-09-068-740A-11	Sequence 11, Appl
1019	116.5	3.7	132	2	US-10-433-794-18	Sequence 18, Appl	1092	114.5	3.7	1218	2	US-09-566-047-2	Sequence 2, Appli
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1021	116.5	3.7	296	2	US-09-270-767-37980	Sequence 37980, A	1094	114.5	3.7	1218	2	US-09-917-254-85	Sequence 85, Appl
1022	116.5	3.7	439	2	US-09-270-767-53197	Sequence 53197, A	1095	114.5	3.7	1218	2	US-09-917-254-85	Sequence 85, Appl
1023	116.5	3.7	943	2	US-10-300-819B-21	Sequence 21, Appl	1096	114.5	3.7	1218	2	US-09-579-536C-1	Sequence 1, Appli
1024	116.5	3.7	943	2	US-08-476-515A-12	Sequence 12, Appl	1097	114.5	3.7	1218	2	US-09-579-536C-1	Sequence 1, Appli
1025	116.5	3.7	1252	2	US-08-652-877-12	Sequence 12, Appl	1098	114.5	3.7	1218	2	US-09-949-016-10297	Sequence 10297, A
1026	116.5	3.7	1252	2	US-09-902-540-13967	Sequence 13967, A	1099	114.5	3.7	1254	2	US-09-949-016-10297	Sequence 53, Appl
1027	116.5	3.7	2887	2	US-08-462-467B-8	Sequence 8, Appli	1100	114	3.6	111	2	US-09-220-528-53	Sequence 29, Appl
1028	116.5	3.7	4654	2	US-08-476-515A-84	Sequence 84, Appl	1101	114	3.6	111	2	US-09-220-528-29	Sequence 16, Appl
1029	116.5	3.7	4655	2	US-08-652-877-84	Sequence 84, Appl	1102	114	3.6	224	2	US-09-347-613C-16	Sequence 16, Appl
1030	116.5	3.7	4655	2	US-08-652-877-88	Sequence 88, Appl	1103	114	3.6	224	2	US-09-662-183A-16	Sequence 16, Appl
1031	116.5	3.7	4655	2	US-08-652-877-90	Sequence 90, Appl	1104	114	3.6	257	2	US-10-101-464A-743	Sequence 743, App
1032	116	3.7	193	2	US-08-652-877-90	Sequence 90, Appl	1105	114	3.6	437	2	US-10-101-464A-743	Sequence 3773, Ap
1033	116	3.7	264	2	US-09-270-767-44942	Sequence 44942, A	1106	114	3.6	631	2	US-10-104-047-3773	Sequence 4123, A
1034	116	3.7	383	2	US-09-252-991A-24670	Sequence 24670, A	1107	114	3.6	644	1	US-09-270-767-44123	Sequence 2, Appli
1035	116	3.7	1053	2	US-10-094-749-2006	Sequence 2006, App	1108	114	3.6	644	2	US-08-866-757-2	Sequence 2, Appli
1036	116	3.7	1181	2	US-09-513-505-8	Sequence 8, Appli	1109	114	3.6	681	2	US-09-153-593-2	Sequence 3586, Ap
1037	116	3.7	1291	2	US-09-826-509-587	Sequence 587, App	1110	114	3.6	875	2	US-10-104-047-3586	Sequence 7, Appli
1038	116	3.7	1291	2	US-09-150-460B-10	Sequence 10, Appl	1111	114	3.6	1063	1	US-09-150-460B-7	Sequence 3, Appli
1039	116	3.7	1291	2	US-08-220-641-5	Sequence 5, Appli	1112	114	3.6	1063	1	US-08-093-453B-3	Sequence 8, Appli
1040	116	3.7	2556	1	US-09-548-473B-1	Sequence 20, Appl	1113	114	3.6	1063	1	US-08-127-499A-8	Sequence 8, Appli
1041	116	3.7	2556	2	US-08-083-590A-20	Sequence 20, Appl	1114	114	3.6	1290	2	US-08-482-847-8	Sequence 8, Appli
1042	115.5	3.7	138	2	US-08-532-384-20	Sequence 4, Appli	1115	114	3.6	1290	2	US-08-400-159-8	Sequence 6, Appli
1043	115.5	3.7	138	2	US-09-191-647-4	Sequence 4, Appli	1116	114	3.6	3571	2	US-09-150-460B-6	Sequence 2, Appli
1044	115.5	3.7	138	2	US-09-540-245A-4	Sequence 4, Appli	1117	114	3.6	3571	2	US-09-911-842A-2	Sequence 2, Appli
1045	115.5	3.7	412	2	US-09-540-153-4	Sequence 4, Appli	1118	114	3.6	3600	2	US-10-037-417-6	Sequence 6, Appli
1046	115.5	3.7	412	2	US-09-289-776-4	Sequence 4, Appli	1119	113.5	3.6	246	2	US-10-037-417-6	Sequence 2, Appli
1047	115.5	3.7	728	2	US-09-252-991A-24484	Sequence 24484, A	1120	113.5	3.6	246	2	US-09-689-486-61	Sequence 61, Appl
1048	115.5	3.7	1093	2	US-09-252-991A-28169	Sequence 28169, A	1121	113.5	3.6	685	2	US-09-973-424A-61	Sequence 61, Appl
					Sequence 55, Appl							US-10-101-464A-918	Sequence 918, App



1122	113.5	3.6	841	2	US-09-252-991A-26919	Sequence 26919, A	1195	111.5	3.6	816	2	US-09-266-225D-12	Sequence 12, Appl
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1124	113.5	3.6	1218	2	US-09-214-278-7	Sequence 7, Appl	1197	111.5	3.6	1021	2	US-10-101-464A-954	Sequence 954, App
1125	113.5	3.6	1218	2	US-09-855-722-7	Sequence 7, Appl	1198	111.5	3.6	1298	1	US-08-690-473-2	Sequence 2, Appl
1126	113	3.6	175	2	US-10-101-464A-801	Sequence 801, Appl	1199	111.5	3.6	1298	1	US-09-259-821A-2	Sequence 2, Appl
1127	113	3.6	681	2	US-09-252-991A-25394	Sequence 25394, A	1200	111.5	3.6	1398	2	US-08-843-659-2	Sequence 2, Appl
1128	113	3.6	369	2	US-10-162-247-2	Sequence 2, Appl	1201	111.5	3.6	1398	2	US-09-825-288A-2	Sequence 2, Appl
1129	113	3.6	688	2	US-09-367-206-20	Sequence 20, Appl	1202	111	3.5	239	2	US-09-252-991A-21250	Sequence 21250, A
1130	113	3.6	688	2	US-09-298-404-20	Sequence 20, Appl	1203	111	3.5	267	2	US-08-818-112-147	Sequence 112, App
1131	113	3.6	723	2	US-10-104-047-2246	Sequence 2246, Ap	1204	111	3.5	267	2	US-08-818-111-137	Sequence 137, App
1132	113	3.6	770	2	US-09-981-953A-2	Sequence 2, Appl	1205	111	3.5	267	2	US-09-056-556-142	Sequence 142, App
1133	113	3.6	979	2	US-09-538-092-990	Sequence 990, App	1206	111	3.5	267	2	US-09-072-596-137	Sequence 137, App
1134	113	3.6	1247	3	US-09-501-171-6	Sequence 6, Appl	1207	111	3.5	267	2	US-09-072-967-142	Sequence 142, App
1135	113	3.6	1717	3	US-09-958-359-20	Sequence 20, Appl	1208	111	3.5	267	2	US-10-193-002-137	Sequence 137, App
1136	113	3.6	1733	3	US-09-958-359-21	Sequence 21, Appl	1209	111	3.5	267	2	US-10-084-843-142	Sequence 142, App
1137	112.5	3.6	328	2	US-09-252-991A-17729	Sequence 17729, A	1210	111	3.5	322	2	US-09-252-991A-29259	Sequence 29259, A
1138	112.5	3.6	677	1	US-08-188-582-13	Sequence 13, Appl	1211	111	3.5	333	2	US-09-252-991A-19956	Sequence 19956, A
1139	112.5	3.6	677	1	US-08-646-715-13	Sequence 13, Appl	1212	111	3.5	452	2	US-09-949-016-7289	Sequence 7289, Ap
1140	112.5	3.6	677	1	US-09-538-092-1164	Sequence 1164, Ap	1213	111	3.5	454	2	US-09-716-964B-5	Sequence 5, Appl
1141	112.5	3.6	694	2	US-09-949-016-8774	Sequence 8774, Ap	1214	111	3.5	492	1	US-08-644-271-32	Sequence 32, Appl
1142	112.5	3.6	694	2	US-09-949-016-8775	Sequence 8775, Ap	1215	111	3.5	492	2	US-09-077-955-36	Sequence 36, Appl
1143	112.5	3.6	711	2	US-09-949-016-8493	Sequence 8493, Ap	1216	111	3.5	492	2	US-10-016-283-36	Sequence 36, Appl
1144	112.5	3.6	825	2	US-10-094-749-3083	Sequence 3083, Ap	1217	111	3.5	595	2	US-09-949-016-7205	Sequence 7205, Ap
1145	112.5	3.6	1068	1	US-08-396-479B-12	Sequence 12, Appl	1218	111	3.5	595	2	US-07-757-342D-2	Sequence 2, Appl
1146	112.5	3.6	1068	1	US-08-818-823-12	Sequence 12, Appl	1219	111	3.5	699	2	US-09-461-657B-2	Sequence 2, Appl
1147	112.5	3.6	1078	2	US-09-949-016-9573	Sequence 9573, Ap	1220	111	3.5	1050	2	US-09-428-711A-16	Sequence 16, Appl
1148	112	3.6	230	2	US-09-252-991A-31737	Sequence 31737, A	1221	111	3.5	1109	2	US-09-949-016-10771	Sequence 10771, A
1149	112	3.6	241	2	US-08-341-018-54	Sequence 54, Appl	1222	111	3.5	1203	2	US-09-949-016-6615	Sequence 6615, Ap
1150	112	3.6	241	2	US-08-470-335-195	Sequence 195, App	1223	111	3.5	1203	2	US-10-067-457-3	Sequence 3, Appl
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1152	112	3.6	241	2	US-08-467-602-389	Sequence 389, App	1225	111	3.5	1358	1	US-08-404-665-4	Sequence 4, Appl
1153	112	3.6	241	2	US-08-411-295F-47	Sequence 47, Appl	1226	111	3.5	1358	1	US-08-404-671-4	Sequence 4, Appl
1154	112	3.6	241	2	US-08-411-295F-94	Sequence 94, Appl	1227	111	3.5	1358	1	US-08-404-781-4	Sequence 4, Appl
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1156	112	3.6	297	1	US-09-262-653A-6	Sequence 6, Appl	1229	111	3.5	1540	2	US-09-949-016-11382	Sequence 11382, A
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1161	112	3.6	404	2	US-10-094-749-3089	Sequence 3089, Ap	1234	111	3.5	1719	2	US-08-516-859A-4	Sequence 4, Appl
1162	112	3.6	417	2	US-09-644-858-5	Sequence 5, Appl	1235	111	3.5	1719	2	US-09-586-472-4	Sequence 4, Appl
1163	112	3.6	417	2	US-09-644-858-8	Sequence 8, Appl	1236	111	3.5	1719	2	US-09-528-706-4	Sequence 4, Appl
1164	112	3.6	422	2	US-09-644-858-13	Sequence 13, Appl	1237	111	3.5	1719	2	US-10-024-450-4	Sequence 4, Appl
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1166	112	3.6	513	1	US-08-480-229C-14	Sequence 14, Appl	1239	111	3.5	2254	2	US-09-949-016-9270	Sequence 9270, Ap
1167	112	3.6	513	1	US-08-659-235C-14	Sequence 14, Appl	1240	111	3.5	2442	2	US-09-514-247A-10	Sequence 10, Appl
1168	112	3.6	720	2	US-09-252-991A-31915	Sequence 31915, A	1241	111	3.5	2442	1	US-09-538-092-1370	Sequence 1370, Ap
1169	112	3.6	750	2	US-09-165-239A-4	Sequence 4, Appl	1242	111	3.5	2523	1	US-08-185-432-18	Sequence 18, Appl
1170	112	3.6	764	2	US-07-757-342D-5	Sequence 5, Appl	1243	111	3.5	2523	2	US-08-899-232-3	Sequence 3, Appl
1171	112	3.6	764	2	US-09-461-657B-5	Sequence 5, Appl	1244	111	3.5	2523	2	US-09-121-457-3	Sequence 3, Appl
1172	112	3.6	764	2	US-09-826-509-395	Sequence 395, App	1245	110.5	3.5	273	2	US-09-252-991A-30433	Sequence 30433, A
1173	112	3.6	764	2	US-09-826-509-399	Sequence 403, App	1246	110.5	3.5	298	2	US-09-248-796A-26762	Sequence 26762, A
1174	112	3.6	764	2	US-09-826-509-403	Sequence 407, App	1247	110.5	3.5	565	2	US-08-937-067-8	Sequence 8, Appl
1175	112	3.6	764	2	US-09-826-509-407	Sequence 411, App	1248	110.5	3.5	645	2	US-09-964-899-17	Sequence 17, Appl
1176	112	3.6	764	2	US-09-826-509-411	Sequence 415, App	1249	110.5	3.5	675	2	US-09-332-063-2	Sequence 2, Appl
1177	112	3.6	764	2	US-09-826-509-415	Sequence 419, App	1250	110.5	3.5	675	2	US-09-332-063-3	Sequence 3, Appl
1178	112	3.6	764	2	US-09-826-509-419	Sequence 423, App	1251	110.5	3.5	708	2	US-09-818-780-76	Sequence 76, Appl
1179	112	3.6	764	2	US-09-826-509-423	Sequence 423, App	1252	110.5	3.5	728	2	US-09-252-991A-31891	Sequence 31891, A
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1181	112	3.6	902	1	US-08-818-823-6	Sequence 6, Appl	1254	110.5	3.5	1207	2	US-09-538-092-1300	Sequence 1300, Ap
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1183	112	3.6	1833	2	US-08-479-722B-2	Sequence 2, Appl	1256	110.5	3.5	1346	2	US-09-320-878-4	Sequence 4, Appl
1184	112	3.6	1833	2	US-09-592-685-2	Sequence 2, Appl	1257	110.5	3.5	1346	2	US-09-105-537-37	Sequence 37, Appl
1185	111.5	3.6	1833	5	PCT-US95-02251-18	Sequence 18, Appl	1258	110.5	3.5	1346	2	US-09-141-908-5	Sequence 5, Appl
1186	111.5	3.6	228	2	US-09-902-540-15349	Sequence 15349, A	1259	110.5	3.5	1346	2	US-09-657-440-4	Sequence 4, Appl
1187	111.5	3.6	281	2	US-09-252-991A-23962	Sequence 23962, A	1260	110.5	3.5	1346	2	US-09-793-708-4	Sequence 4, Appl
1188	111.5	3.6	281	2	US-10-101-464A-619	Sequence 619, App	1261	110.5	3.5	1384	2	US-08-976-255-11	Sequence 11, Appl
1189	111.5	3.6	320	2	US-09-252-991A-21056	Sequence 21056, A	1262	110.5	3.5	1656	2	US-09-949-016-7247	Sequence 7247, Ap
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1191	111.5	3.6	417	2	US-09-949-016-11098	Sequence 11098, A	1264	110.5	3.5	3724	1	US-08-804-227C-10	Sequence 10, Appl
1192	111.5	3.6	417	2	US-09-949-002-548	Sequence 548, App	1265	110.5	3.5	3724	1	US-08-804-198-4	Sequence 4, Appl
1193	111.5	3.6	445	2	US-09-252-991A-22368	Sequence 22368, A	1266	110.5	3.5	11877	2	US-09-105-537-6	Sequence 6, Appl
1194	111.5	3.6	766	2	US-09-902-540-10602	Sequence 10602, A	1267	110	3.5	195	2	US-09-858-664A-11	Sequence 11, Appl



1268	110	3.5	195	2	US-10-274-978-12	Sequence 12, Appl	1341	109	3.5	833	1	US-08-346-126-6	Sequence 6, Appl
1269	110	3.5	195	2	US-10-697-263-12	Sequence 12, Appl	1342	109	3.5	833	1	US-08-346-128-6	Sequence 6, Appl
1270	110	3.5	450	2	US-09-369-364A-19	Sequence 19, Appl	1343	109	3.5	833	2	US-08-532-384-2	Sequence 2, Appl
1271	110	3.5	626	2	US-09-345-473E-43	Sequence 43, Appl	1344	109	3.5	833	2	US-08-893-828-6	Sequence 6, Appl
1272	110	3.5	626	2	US-09-862-027-43	Sequence 43, Appl	1345	109	3.5	850	1	US-08-286-305A-7	Sequence 7, Appl
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1274	110	3.5	739	2	US-09-035-648-24	Sequence 24, Appl	1347	109	3.5	850	1	US-08-440-816A-7	Sequence 7, Appl
1275	110	3.5	739	2	US-09-001-951-24	Sequence 24, Appl	1348	109	3.5	850	2	US-08-417-381A-7	Sequence 7, Appl
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1277	110	3.5	746	2	US-09-548-797B-4	Sequence 19, Appl	1350	109	3.5	883	2	US-10-195-970-3	Sequence 6, Appl
1278	110	3.5	2703	2	US-08-185-432-19	Sequence 19, Appl	1351	109	3.5	883	2	US-10-195-970-6	Sequence 167, App
1279	110	3.5	2703	2	US-08-899-232-4	Sequence 4, Appl	1352	109	3.5	1145	1	US-09-758-759-167	Sequence 58, Appl
1280	110	3.5	2703	2	US-09-121-457-4	Sequence 4, Appl	1353	109	3.5	1336	1	US-08-231-193A-58	Sequence 58, Appl
1281	109.5	3.5	297	2	US-09-252-991A-32590	Sequence 32590, A	1354	109	3.5	1336	1	US-08-486-273A-58	Sequence 58, Appl
1282	109.5	3.5	343	2	US-10-101-464A-892	Sequence 892, App	1355	109	3.5	1336	2	US-08-940-086A-58	Sequence 58, Appl
1283	109.5	3.5	381	2	US-10-101-464A-660	Sequence 660, App	1356	109	3.5	1336	2	US-08-940-035A-58	Sequence 58, Appl
1284	109.5	3.5	400	2	US-10-101-464A-939	Sequence 939, App	1357	109	3.5	1336	2	US-08-935-105A-58	Sequence 58, Appl
1285	109.5	3.5	401	7	5252556-1	Patent No. 5252556	1358	109	3.5	1336	2	US-09-648-797-58	Sequence 58, Appl
1286	109.5	3.5	456	2	US-08-470-335-246	Sequence 246, App	1359	109	3.5	1336	2	US-09-386-123-58	Sequence 58, Appl
1287	109.5	3.5	456	2	US-08-467-602-303	Sequence 303, App	1360	109	3.5	1336	2	US-10-038-937-58	Sequence 58, Appl
1288	109.5	3.5	456	2	US-08-411-295F-229	Sequence 229, App	1361	109	3.5	1336	2	US-10-007-747-58	Sequence 58, Appl
1289	109.5	3.5	490	2	US-08-467-602-345	Sequence 345, App	1362	109	3.5	1336	2	US-09-945-901-58	Sequence 58, Appl
1290	109.5	3.5	490	2	US-08-411-295F-271	Sequence 271, App	1363	109	3.5	1358	2	US-09-949-002-353	Sequence 353, App
1291	109.5	3.5	612	1	US-08-359-705B-8	Sequence 8, Appl	1364	109	3.5	1385	2	US-09-270-767-32762	Sequence 431, App
1292	109.5	3.5	612	1	US-08-286-846A-8	Sequence 8, Appl	1365	108.5	3.5	74	2	US-09-270-767-32762	Sequence 32762, A
1293	109.5	3.5	612	1	US-08-457-880A-8	Sequence 8, Appl	1366	108.5	3.5	74	2	US-09-270-767-47979	Sequence 47979, A
1294	109.5	3.5	612	2	US-08-444-622A-8	Sequence 8, Appl	1367	108.5	3.5	269	2	US-09-902-540-16596	Sequence 16596, A
1295	109.5	3.5	612	2	US-08-942-562-8	Sequence 8, Appl	1368	108.5	3.5	288	2	US-09-252-991A-32807	Sequence 32807, A
1296	109.5	3.5	612	2	US-09-156-923-8	Sequence 8, Appl	1369	108.5	3.5	381	2	US-09-510-031A-5	Sequence 5, Appl
1297	109.5	3.5	632	2	US-09-252-991A-25544	Sequence 25544, A	1370	108.5	3.5	404	2	US-09-550-115-11	Sequence 11, Appl
1298	109.5	3.5	690	2	US-09-228-986-69	Sequence 69, Appl	1371	108.5	3.5	514	2	US-09-712-363-154	Sequence 154, App
1299	109.5	3.5	690	2	US-10-101-464A-69	Sequence 7806, Ap	1372	108.5	3.5	542	2	US-09-252-991A-21862	Sequence 21862, A
1300	109.5	3.5	693	2	US-09-949-016-7806	Sequence 940, App	1373	108.5	3.5	548	1	US-08-468-576B-19	Sequence 19, Appl
1301	109.5	3.5	697	2	US-10-101-464A-940	Sequence 12, Appl	1374	108.5	3.5	548	1	US-08-468-577B-19	Sequence 19, Appl
1302	109.5	3.5	784	2	US-09-004-838-12	Sequence 8, Appl	1375	108.5	3.5	548	2	US-08-468-740A-9	Sequence 9, Appl
1303	109.5	3.5	798	2	US-09-150-460B-8	Sequence 6, Appl	1376	108.5	3.5	702	2	US-09-068-740A-9	Sequence 9, Appl
1304	109.5	3.5	839	1	US-08-359-705B-6	Sequence 6, Appl	1377	108.5	3.5	723	2	US-09-423-753-27	Sequence 27, Appl
1305	109.5	3.5	839	1	US-08-286-846A-6	Sequence 6, Appl	1378	108.5	3.5	723	3	US-10-241-476-27	Sequence 27, Appl
1306	109.5	3.5	839	1	US-08-457-880A-6	Sequence 6, Appl	1379	108.5	3.5	825	1	US-07-912-952-2	Sequence 2, Appl
1307	109.5	3.5	839	2	US-08-444-622A-6	Sequence 6, Appl	1380	108.5	3.5	907	2	US-09-248-796A-17307	Sequence 17307, A
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1310	109.5	3.5	904	2	US-09-252-991A-25286	Sequence 25286, A	1383	108.5	3.5	1125	2	US-09-430-656-152	Sequence 152, App
1311	109.5	3.5	1235	2	US-09-949-016-8455	Sequence 8455, Ap	1384	108.5	3.5	1125	2	US-10-100-957A-152	Sequence 152, App
1312	109.5	3.5	1235	2	US-09-949-016-8456	Sequence 8456, Ap	1385	108.5	3.5	1125	2	US-09-266-225D-18	Sequence 18, App
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1315	109	3.5	221	1	US-08-659-235C-29	Sequence 29, Appl	1388	108.5	3.5	1527	2	US-09-513-783A-22	Sequence 22, Appl
1316	109	3.5	259	2	US-10-094-749-2303	Sequence 2303, Ap	1389	108.5	3.5	1610	2	US-09-430-656-22	Sequence 22, Appl
1317	109	3.5	416	2	US-08-978-289-12	Sequence 12, Appl	1390	108.5	3.5	1610	2	US-10-100-957A-22	Sequence 22, Appl
1318	109	3.5	416	2	US-09-601-478-1	Sequence 1, Appl	1391	108.5	3.5	1610	2	US-09-964-956-66	Sequence 66, Appl
1319	109	3.5	416	2	US-09-601-478-4	Sequence 4, Appl	1392	108.5	3.5	51	2	US-10-037-417-100	Sequence 100, App
1320	109	3.5	433	2	US-09-252-991A-29241	Sequence 29241, A	1393	108	3.4	51	2	US-09-210A-1	Sequence 1, Appl
1321	109	3.5	437	1	US-08-136-119-2	Sequence 2, Appl	1394	108	3.4	152	2	US-09-113-825-1	Sequence 3, Appl
1322	109	3.5	437	1	US-08-481-814A-7	Sequence 7, Appl	1395	108	3.4	180	2	US-09-287-354-3	Sequence 3, Appl
1323	109	3.5	437	1	US-09-252-991A-32620	Sequence 32620, A	1396	108	3.4	180	2	US-10-024-368-3	Sequence 3, Appl
1324	109	3.5	437	2	US-09-949-002-540	Sequence 10, Appl	1397	108	3.4	419	2	US-10-164-595-58	Sequence 58, Appl
1325	109	3.5	480	1	US-08-480-229C-10	Sequence 10, Appl	1398	108	3.4	419	2	US-09-949-016-10827	Sequence 4, Appl
1326	109	3.5	480	1	US-08-659-235C-10	Sequence 10, Appl	1399	108	3.4	590	1	US-09-298-404-5	Sequence 5, Appl
1327	109	3.5	507	2	US-09-599-287A-24	Sequence 24, Appl	1400	108	3.4	618	2	US-09-902-540-11260	Sequence 11260, A
1328	109	3.5	507	2	US-10-078-547-24	Sequence 24, Appl	1401	108	3.4	703	2	US-09-252-991A-23373	Sequence 23373, A
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1330	109	3.5	552	2	US-09-252-991A-23036	Sequence 23036, A	1403	108	3.4	820	2	US-09-113-825-1	Sequence 3, Appl
1331	109	3.5	560	2	US-09-252-991A-25999	Sequence 25999, A	1404	108	3.4	820	2	US-09-287-354-3	Sequence 3, Appl
1332	109	3.5	730	2	US-09-252-991A-25999	Sequence 25999, A	1405	108	3.4	820	2	US-10-164-595-58	Sequence 58, Appl
1333	109	3.5	749	2	US-09-828-313-27	Sequence 27, Appl	1406	108	3.4	1015	1	US-09-949-016-10827	Sequence 4, Appl
1334	109	3.5	762	1	US-08-642-255-114	Sequence 114, App	1407	108	3.4	1015	1	US-08-462-467B-4	Sequence 4, Appl
1335	109	3.5	762	1	US-08-397-633A-26	Sequence 26, Appl	1408	108	3.4	1189	2		
1336	109	3.5	764	2	US-09-186-350A-53	Sequence 53, Appl	1409	108	3.4	1189	2		
1337	109	3.5	828	2	US-10-101-464A-934	Sequence 934, App	1410	108	3.4	1320	2		
1338	109	3.5	833	1	US-08-264-534-6	Sequence 6, Appl	1411	108	3.4	1404	2		
1339	109	3.5	833	1	US-08-083-590A-2	Sequence 2, Appl	1412	108	3.4	1411	2		
1340	109	3.5	833	1	US-08-465-500-6	Sequence 6, Appl	1413	108	3.4	1618	2		







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Db 541 GPCAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGLQSPHAKPYI 598

RESULT 2

US-09-944-457-69  
; Sequence 69, Application US/09944457  
; Patent No. 6734288  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Baton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,457  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 69  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-944-457-69

Query Match 100.0%; Score 3135; DB 2; Length 598;  
Best Local Similarity 100.0%; Pred. No. 7.3e-217;  
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MCSRVPLLLPLLLLLALGPGVQGCPCGCQCSCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60  
Db 1 MCSRVPLLLPLLLLLALGPGVQGCPCGCQCSCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60  
QY 61 ENGITMLDASSFAGLPGLQLLLDLSQNOIASIRLPRLLLLSHNSHLALPGILDANVE 120  
Db 61 ENGITMLDASSFAGLPGLQLLLDLSQNOIASIRLPRLLLLSHNSHLALPGILDANVE 120



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QY 121 ALRLAGLGLQOQDEGLFSLRLNLHLDVSDNQLERVPVIRGLRGLTRLRLAGNTRIAQL 180
Db 121 ALRLAGLGLQOQDEGLFSLRLNLHLDVSDNQLERVPVIRGLRGLTRLRLAGNTRIAQL 180
QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLGSLFPLRLLLAAARNPNCVCPPLSWFGFWVRE 240
Db 181 RPEDLAGLAALQELDVSNLSLOALPGDLGSLFPLRLLLAAARNPNCVCPPLSWFGFWVRE 240
QY 241 SHVTLASPETRCHFPKPNAGRLLELDYADVGCCPATTTATVTPTRPVVREPTALSSSL 300
Db 241 SHVTLASPETRCHFPKPNAGRLLELDYADVGCCPATTTATVTPTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPSTCLNGSTCHLGRHHLACLCPGG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPSTCLNGSTCHLGRHHLACLCPGG 360
QY 361 FTGLYESQMGOGTRPSPTPTVTPRPRSLTLGIEPVSTSLRVGLQRYLQSSVQLRSRLR 420
Db 361 FTGLYESQMGOGTRPSPTPTVTPRPRSLTLGIEPVSTSLRVGLQRYLQSSVQLRSRLR 420
QY 421 LTYRNLSGDKRLVTLRLPASLAETVTVTLRPNATYSVCVMPGLGPRVPEGEACEAHT 480
Db 421 LTYRNLSGDKRLVTLRLPASLAETVTVTLRPNATYSVCVMPGLGPRVPEGEACEAHT 480
QY 481 PPAVSHNSHAPVTOAREGNLPLLIAPALAAVLAALAAVCAAYCVRRGRAMAAAOQKGOV 540
Db 481 PPAVSHNSHAPVTOAREGNLPLLIAPALAAVLAALAAVCAAYCVRRGRAMAAAOQKGOV 540
QY 541 GFGAGFLELEGVKVPLEPGPKATEGGEGALPGSGSECEVPLMGFPFGQLSPHAKPYI 598
Db 541 GFGAGFLELEGVKVPLEPGPKATEGGEGALPGSGSECEVPLMGFPFGQLSPHAKPYI 598

RESULT 3
US-09-945-584-69
; Sequence 69, Application US/09945584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,584
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
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Query Match 100.0%; Score 3135; DB 2: Length 598;
Best Local Similarity 100.0%; Pred. No. 7.3e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MCSRVPLLLPLLLLLALGFGVGCSPGCGCQSQPQTVFCTARQTTVPDRDPTVGLVVF 60  
DB 1 MCSRVPLLLPLLLLLALGFGVGCSPGCGCQSQPQTVFCTARQTTVPDRDPTVGLVVF 60  
QY 61 ENGITWLDASSFAGLPGQLQLDLSQNIASLRLPRLLLLDLSHNLLALEPGILDITANVE 120  
DB 61 ENGITWLDASSFAGLPGQLQLDLSQNIASLRLPRLLLLDLSHNLLALEPGILDITANVE 120  
QY 121 ALRLAGLGLQOLDEGLFSLRNLHDLVDSDNOLERVPPVIRGLRGLTLRLAGNTRIAQL 180  
DB 121 ALRLAGLGLQOLDEGLFSLRNLHDLVDSDNOLERVPPVIRGLRGLTLRLAGNTRIAQL 180  
QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLFPRLRLAAARNPNCVPLSWFGFVWRE 240  
DB 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLFPRLRLAAARNPNCVPLSWFGFVWRE 240  
QY 241 SHVTLASPETRCHFPKKNAGRLLELDVADFGCPATTTTATVTPTRPVVREPTALSSSL 300  
DB 241 SHVTLASPETRCHFPKKNAGRLLELDVADFGCPATTTTATVTPTRPVVREPTALSSSL 300  
QY 301 APTWLSPTAPATEAPSPSTAPTPTGVPQPODCPSTCLNGTCHLGRHHLACLCPBG 360  
DB 301 APTWLSPTAPATEAPSPSTAPTPTGVPQPODCPSTCLNGTCHLGRHHLACLCPBG 360  
QY 361 FTGLYCESQMGQTRPSPTPTPRPRSLTLGIEPVSPSTSLRVGLQRYLQSSVQLRSUR 420  
DB 361 FTGLYCESQMGQTRPSPTPTPRPRSLTLGIEPVSPSTSLRVGLQRYLQSSVQLRSUR 420  
QY 421 LTVRNLSGDPDKRLVTURLPASLAETVTVQLRPNATYSVCVMPDLPGRVPEGEACGEAHT 480  
DB 421 LTVRNLSGDPDKRLVTURLPASLAETVTVQLRPNATYSVCVMPDLPGRVPEGEACGEAHT 480  
QY 481 PPAVHNSHAPVTOAREGNPLLTAPALAAVLAALAAVGAAYCVRGRMAAAAOBKGV 540  
DB 481 PPAVHNSHAPVTOAREGNPLLTAPALAAVLAALAAVGAAYCVRGRMAAAAOBKGV 540  
QY 541 GPAGPGLGKGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPPLHAKPYI 598  
DB 541 GPAGPGLGKGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPPLHAKPYI 598  
RESULT 4  
US-09-944-944-69  
; Sequence 69, Application US/09944944  
; Patent No. 6929947  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijavini, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944, 944  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866, 028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067, 411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 686  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069, 873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068, 017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070, 440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074, 086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074, 092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075, 945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112, 850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113, 296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146, 222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216, 021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218, 517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254, 311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6929947ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6929947ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 69  
; LENGTH: 598







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; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-69

Query Match      100.0%; Score 3135; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 7.3e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVP LLLP LLL L L L L L A L G P G V G C P S G C C Q S Q P Q T V F C T A R Q G T T V P R D V P D T V G L Y V F 60
Db 1 MCSRVP LLLP LLL L L L L A L G P G V G C P S G C C Q S Q P Q T V F C T A R Q G T T V P R D V P D T V G L Y V F 60
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Db 61 ENGITWLDASSFAGLPGLQLLDLSQNQIASRLPRLLDLDSHNSLLALEPGILDNTANVE 120
QY 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDNQLERVPVIRGLRGLRTRLRAGNTRIAQL 180
Db 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDNQLERVPVIRGLRGLRTRLRAGNTRIAQL 180
QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLGSLFRLRLAARNPFCVPLSWFGPWVRE 240
Db 181 RPEDLAGLAALQELDVSNLSLOALPGDLGSLFRLRLAARNPFCVPLSWFGPWVRE 240
QY 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
QY 361 FTGLYCESQMGQTRPSPTVTPRPSRLTLGIEPVSPSLRVLQRYLOGSSVQLRSLR 420
Db 361 FTGLYCESQMGQTRPSPTVTPRPSRLTLGIEPVSPSLRVLQRYLOGSSVQLRSLR 420
QY 421 LTVRNLSGPDKRLVTLRLPASLAETVTLQLRPNATYSVCMPLGPGRVPEGEACGEAHT 480
Db 421 LTVRNLSGPDKRLVTLRLPASLAETVTLQLRPNATYSVCMPLGPGRVPEGEACGEAHT 480
QY 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPPLHAKPYI 598
Db 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPPLHAKPYI 598

RESULT 6
US-09-944-884-69
; Sequence 69, Application US/09944884
; Patent No. 7018837
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/09/944,884
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-884-69

Query Match      100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 7.3e-217;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVP LLLP LLL L L L L L A L G P G V G C P S G C C Q S Q P Q T V F C T A R Q G T T V P R D V P D T V G L Y V F 60
Db 1 MCSRVP LLLP LLL L L L L L A L G P G V G C P S G C C Q S Q P Q T V F C T A R Q G T T V P R D V P D T V G L Y V F 60
QY 61 ENGITWLDASSFAGLPGLQLLDLSQNQIASRLPRLLDLDSHNSLLALEPGILDNTANVE 120
Db 61 ENGITWLDASSFAGLPGLQLLDLSQNQIASRLPRLLDLDSHNSLLALEPGILDNTANVE 120
QY 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDNQLERVPVIRGLRGLRTRLRAGNTRIAQL 180
Db 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDNQLERVPVIRGLRGLRTRLRAGNTRIAQL 180
QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLGSLFRLRLAARNPFCVPLSWFGPWVRE 240
Db 181 RPEDLAGLAALQELDVSNLSLOALPGDLGSLFRLRLAARNPFCVPLSWFGPWVRE 240
QY 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
Db 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVQPCPPSTCLNGGTCCHLGRHHLACLCEG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVQPCPPSTCLNGGTCCHLGRHHLACLCEG 360
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Db 361 FTGLYCESQMGQTRPSPTVTPRPSRLTLGIEPVSPSLRVLQRYLOGSSVQLRSLR 420
QY 421 LTVRNLSGPDKRLVTLRLPASLAETVTLQLRPNATYSVCMPLGPGRVPEGEACGEAHT 480
Db 421 LTVRNLSGPDKRLVTLRLPASLAETVTLQLRPNATYSVCMPLGPGRVPEGEACGEAHT 480
QY 481 PPAVHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGV 540
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QY 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPPLHAKPYI 598
Db 541 GPGAGPLEGKVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPPLHAKPYI 598

RESULT 7
US-09-063-950-2
; Sequence 2, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: MEI-019
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RESULT 8  
US-09-991-181-52  
; Sequence 52, Application US/09991181  
; Patent No. 6913919  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bostein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.

APPLICANT:	Ferrara, Napoleone	US/09/09/9	FILE REFERENCE: P2730P1C53
APPLICANT:	Pong, Sherman	PRIOR APPLICATION NUMBER: 60/049787	CURRENT FILING DATE: 2001-11-16
APPLICANT:	Gerber, Hanspeter	PRIOR FILING DATE: 1997-06-16	PRIOR APPLICATION NUMBER: 60/062250
APPLICANT:	Gerritsen, Mary E.	PRIOR FILING DATE: 1997-10-17	PRIOR APPLICATION NUMBER: 60/065186
APPLICANT:	Goddard, Audrey	PRIOR FILING DATE: 1997-11-12	PRIOR APPLICATION NUMBER: 60/065311
APPLICANT:	Godowski, Paul J.	PRIOR FILING DATE: 1997-11-13	PRIOR APPLICATION NUMBER: 60/066770
APPLICANT:	Grimaldi, J. Christopher	PRIOR FILING DATE: 1997-11-24	PRIOR APPLICATION NUMBER: 60/075945
APPLICANT:	Klujvein, Austin L.	PRIOR FILING DATE: 1998-02-25	PRIOR APPLICATION NUMBER: 60/078910
APPLICANT:	Klujvein, Ivar J.	PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/083322
APPLICANT:	Napier, Mary A.	PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/084600
APPLICANT:	Pan, James	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/087106
APPLICANT:	Pan, Nicholas F.	PRIOR FILING DATE: 1998-05-28	PRIOR APPLICATION NUMBER: 60/087607
APPLICANT:	Roy, Margaret Ann	PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087609
APPLICANT:	Stewart, Timothy A.	PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087759
APPLICANT:	Tumas, Daniel	PRIOR FILING DATE: 1998-06-02	PRIOR APPLICATION NUMBER: 60/087827
APPLICANT:	Watanabe, Colin K.	PRIOR FILING DATE: 1998-06-03	PRIOR APPLICATION NUMBER: 60/088021
APPLICANT:	Williams, P. Mickey	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088025
APPLICANT:	Wood, William I.	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088026
APPLICANT:	Zhang, Zemin	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088028
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TITLE OF INVENTION:	Acids Encoding	PRIOR FILING DATE: 1998-06-04	PRIOR APPLICATION NUMBER: 60/088030
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US-09-990-444-52  
; Sequence 52, Application US/09990444  
; Patent No. 6930170  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C19  
; CURRENT APPLICATION NUMBER: US/09/990,444  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
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APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC27  
CURRENT APPLICATION NUMBER: US/09/997,333  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: 60/049787  
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Db 121 RGLRRLRLYLGNRIHQGAFTDLRLLELKLQDNEIRALPPLRLPRELLLLDLSHNS 180  
  
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; PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 3; Length 673;  
Best Local Similarity 88.7%; Pred. No. 4.2e-213;  
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; Patent No. 7019116  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.



APPLICANT: Botstein, David  
APPLICANT: Desmoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC46  
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Db	361	TRPVUREPTALSSSLAPTWSPTATAPSPSTAPPTVGVPOPODCPSTCLNGGTC	420
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QY	526	RGRAAAAQDKGVGPGAGPLEGKVPLEPGKATEGGGEALPSGSECEVPLMGFPF	585
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; Sequence 52, Application US/09989728			
; Patent No. 7029873			
; GENERAL INFORMATION:			
; APPLICANT: Ashkenazi, Avi J.			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Kijavini, Ivar J.			
; APPLICANT: Napier, Mary A.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; FILE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: P27301C72			
; CURRENT APPLICATION NUMBER: US/09/989,728			
; CURRENT FILING DATE: 2001-11-20			
; PRIOR APPLICATION NUMBER: 60/049787			
; PRIOR FILING DATE: 1997-06-16			
; PRIOR APPLICATION NUMBER: 60/062250			
; PRIOR FILING DATE: 1997-10-17			
; PRIOR APPLICATION NUMBER: 60/065186			
; PRIOR FILING DATE: 1997-11-12			
; PRIOR APPLICATION NUMBER: 60/065311			
; PRIOR FILING DATE: 1997-11-13			
; PRIOR APPLICATION NUMBER: 60/066770			

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Db	1	MCSRPVLLPPLLLALGFGVCGSCGCSQPTVCTARQGTTPVPRDVPDDTVGLYVF	60
QY	61	ENGITWLDASSFAGLPGLLLDLSNQIAS	90
Db	61	ENGITWLDASSFAGLPGLLLDLSNQIAS	120
QY	91	-----LRLPRLLLDLSHNS	105
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QY	106	LLALPGLDTPANVEALRLAGLQGLDEGLFSRLNLHDLVDSONQLERVPVIRGLRG	165
Db	181	LLALPGLDTPANVEALRLAGLQGLDEGLFSRLNLHDLVDSONQLERVPVIRGLRG	240
QY	166	LTELRLAGNTRIAQURPEDLAGLALQELVDNSLSQALPGDLSGLFPLRLIAARNPF	225
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Query Match 98.4%; Score 3083.5; DB 3; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 4.2e-213;  
 Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;



[illegible]



; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091626  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 98.4%; Score 3083.5; DB 3; Length 673;  
Best Local Similarity 88.7%; Pred. No. 4.2e-213;  
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;  
  
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DB 61 ENGITWLDAGSFAGLQQLDLSQNOIASLPSGVFOPLANLSNLDLTANRLHEITNETF 120  
  
QY 91 -----LRLPRLLLDLSHNS 105  
DB 121 RGLRRLRLYLGKNIIRHIQCAFDTDLRLLEKLQDNELRALPLRLPRLLLDLSHNS 180  
  
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Search completed: July 27, 2006, 12:11:33  
Job time : 66 secs



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131	3135	100.0	598	5	US-10-858-993-69	Sequence 69, Appl	204	3083.5	98.4	673	3	US-09-998-041-52	Sequence 52, Appl
132	3135	100.0	598	5	US-10-901-400-69	Sequence 69, Appl	205	3083.5	98.4	673	3	US-09-997-585-52	Sequence 52, Appl
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158	3083.5	98.4	673	3	US-09-990-444-52	Sequence 52, Appl	231	3083.5	98.4	673	4	US-10-063-567-16	Sequence 16, Appl
159	3083.5	98.4	673	3	US-09-991-181-52	Sequence 52, Appl	232	3083.5	98.4	673	4	US-10-063-538-16	Sequence 16, Appl
160	3083.5	98.4	673	3	US-09-989-730-52	Sequence 52, Appl	233	3083.5	98.4	673	4	US-10-063-599-16	Sequence 16, Appl
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164	3083.5	98.4	673	3	US-09-997-653-52	Sequence 52, Appl	237	3083.5	98.4	673	4	US-10-063-585-16	Sequence 16, Appl
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168	3083.5	98.4	673	3	US-09-993-667-52	Sequence 52, Appl	241	3083.5	98.4	673	4	US-10-063-586-16	Sequence 16, Appl
169	3083.5	98.4	673	3	US-09-997-428-52	Sequence 52, Appl	242	3083.5	98.4	673	4	US-10-063-546-16	Sequence 16, Appl
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248	3083.5	98.4	673	4	US-10-063-670-16	Sequence 16, Appl	321	3083.5	98.4	673	4	US-10-063-602-16	Sequence 16, Appl
249	3083.5	98.4	673	4	US-10-063-671-16	Sequence 16, Appl	322	3083.5	98.4	673	4	US-10-063-606-16	Sequence 16, Appl
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252	3083.5	98.4	673	4	US-10-063-676-16	Sequence 16, Appl	325	3083.5	98.4	673	4	US-10-063-614-16	Sequence 16, Appl
253	3083.5	98.4	673	4	US-10-063-686-16	Sequence 16, Appl	326	3083.5	98.4	673	4	US-10-063-639-16	Sequence 16, Appl
254	3083.5	98.4	673	4	US-10-063-689-16	Sequence 16, Appl	327	3083.5	98.4	673	4	US-10-063-643-16	Sequence 16, Appl
255	3083.5	98.4	673	4	US-10-063-692-16	Sequence 16, Appl	328	3083.5	98.4	673	4	US-10-063-646-16	Sequence 16, Appl
256	3083.5	98.4	673	4	US-10-063-693-16	Sequence 16, Appl	329	3083.5	98.4	673	4	US-10-063-651-16	Sequence 16, Appl
257	3083.5	98.4	673	4	US-10-063-694-16	Sequence 16, Appl	330	3083.5	98.4	673	4	US-10-063-653-16	Sequence 16, Appl
258	3083.5	98.4	673	4	US-10-063-698-16	Sequence 16, Appl	331	3083.5	98.4	673	4	US-10-063-660-16	Sequence 16, Appl
259	3083.5	98.4	673	4	US-10-063-699-16	Sequence 16, Appl	332	3083.5	98.4	673	4	US-10-063-665-16	Sequence 16, Appl
260	3083.5	98.4	673	4	US-10-063-702-16	Sequence 16, Appl	333	3083.5	98.4	673	4	US-10-063-584-16	Sequence 16, Appl
261	3083.5	98.4	673	4	US-10-063-705-16	Sequence 16, Appl	334	3083.5	98.4	673	4	US-10-063-536-16	Sequence 16, Appl
262	3083.5	98.4	673	4	US-10-063-707-16	Sequence 16, Appl	335	3083.5	98.4	673	4	US-10-063-562-16	Sequence 16, Appl
263	3083.5	98.4	673	4	US-10-063-709-16	Sequence 16, Appl	336	3083.5	98.4	673	4	US-10-063-638-16	Sequence 16, Appl
264	3083.5	98.4	673	4	US-10-063-713-16	Sequence 16, Appl	337	3083.5	98.4	673	4	US-10-063-666-16	Sequence 16, Appl
265	3083.5	98.4	673	4	US-10-063-722-16	Sequence 16, Appl	338	3083.5	98.4	673	4	US-10-063-672-16	Sequence 16, Appl
266	3083.5	98.4	673	4	US-10-063-727-16	Sequence 16, Appl	339	3083.5	98.4	673	4	US-10-063-682-16	Sequence 16, Appl
267	3083.5	98.4	673	4	US-10-063-730-16	Sequence 16, Appl	340	3083.5	98.4	673	4	US-10-063-721-16	Sequence 16, Appl
268	3083.5	98.4	673	4	US-10-063-734-16	Sequence 16, Appl	341	3083.5	98.4	673	4	US-10-063-723-16	Sequence 16, Appl
269	3083.5	98.4	673	4	US-10-063-736-16	Sequence 16, Appl	342	3083.5	98.4	673	4	US-10-063-514-16	Sequence 16, Appl
270	3083.5	98.4	673	4	US-10-063-742-16	Sequence 16, Appl	343	3083.5	98.4	673	4	US-10-063-516-16	Sequence 16, Appl
271	3083.5	98.4	673	4	US-10-063-743-16	Sequence 16, Appl	344	3083.5	98.4	673	4	US-10-063-529-16	Sequence 16, Appl
272	3083.5	98.4	673	4	US-10-063-744-16	Sequence 16, Appl	345	3083.5	98.4	673	4	US-10-063-688-16	Sequence 16, Appl
273	3083.5	98.4	673	4	US-10-063-565-16	Sequence 16, Appl	346	3083.5	98.4	673	4	US-10-063-684-16	Sequence 16, Appl
274	3083.5	98.4	673	4	US-10-063-577-16	Sequence 16, Appl	347	3083.5	98.4	673	4	US-10-063-520-16	Sequence 16, Appl
275	3083.5	98.4	673	4	US-10-063-591-16	Sequence 16, Appl	348	3083.5	98.4	673	4	US-10-063-647-16	Sequence 16, Appl
276	3083.5	98.4	673	4	US-10-063-610-16	Sequence 16, Appl	349	3083.5	98.4	673	4	US-10-063-548-16	Sequence 16, Appl
277	3083.5	98.4	673	4	US-10-063-673-16	Sequence 16, Appl	350	3083.5	98.4	673	4	US-10-063-578-16	Sequence 16, Appl
278	3083.5	98.4	673	4	US-10-063-710-16	Sequence 16, Appl	351	3083.5	98.4	673	4	US-10-063-648-16	Sequence 16, Appl
279	3083.5	98.4	673	4	US-10-063-711-16	Sequence 16, Appl	352	3083.5	98.4	673	4	US-10-063-677-16	Sequence 16, Appl
280	3083.5	98.4	673	4	US-10-063-712-16	Sequence 16, Appl	353	3083.5	98.4	673	4	US-10-063-718-16	Sequence 16, Appl
281	3083.5	98.4	673	4	US-10-063-714-16	Sequence 16, Appl	354	3083.5	98.4	673	4	US-10-063-741-16	Sequence 16, Appl
282	3083.5	98.4	673	4	US-10-063-715-16	Sequence 16, Appl	355	3083.5	98.4	673	4	US-10-063-617-16	Sequence 16, Appl
283	3083.5	98.4	673	4	US-10-063-716-16	Sequence 16, Appl	356	3083.5	98.4	673	4	US-10-063-664-16	Sequence 16, Appl
284	3083.5	98.4	673	4	US-10-063-717-16	Sequence 16, Appl	357	3083.5	98.4	673	4	US-10-063-561-16	Sequence 16, Appl
285	3083.5	98.4	673	4	US-10-063-720-16	Sequence 16, Appl	358	3083.5	98.4	673	4	US-10-063-618-16	Sequence 16, Appl
286	3083.5	98.4	673	4	US-10-063-722-16	Sequence 16, Appl	359	3083.5	98.4	673	4	US-10-063-657-16	Sequence 16, Appl
287	3083.5	98.4	673	4	US-10-063-726-16	Sequence 16, Appl	360	3083.5	98.4	673	4	US-10-063-668-16	Sequence 16, Appl
288	3083.5	98.4	673	4	US-10-063-728-16	Sequence 16, Appl	361	3083.5	98.4	673	4	US-10-219-538-52	Sequence 52, Appl
289	3083.5	98.4	673	4	US-10-063-731-16	Sequence 16, Appl	362	3083.5	98.4	673	4	US-10-063-743-52	Sequence 52, Appl
290	3083.5	98.4	673	4	US-10-063-732-16	Sequence 16, Appl	363	3083.5	98.4	673	4	US-10-063-018-59	Sequence 59, Appl
291	3083.5	98.4	673	4	US-10-063-523-16	Sequence 16, Appl	364	3083.5	98.4	673	5	US-10-972-317-16	Sequence 16, Appl
292	3083.5	98.4	673	4	US-10-063-527-16	Sequence 16, Appl	365	3083.5	98.4	673	5	US-10-950-374-52	Sequence 52, Appl
293	3083.5	98.4	673	4	US-10-063-579-16	Sequence 16, Appl	366	3083.5	98.4	673	5	US-10-063-703-16	Sequence 16, Appl
294	3083.5	98.4	673	4	US-10-063-581-16	Sequence 16, Appl	367	3083.5	98.4	673	6	US-11-102-240-16	Sequence 16, Appl
295	3083.5	98.4	673	4	US-10-063-583-16	Sequence 16, Appl	368	3083.5	98.4	673	6	US-11-103-193-16	Sequence 16, Appl
296	3083.5	98.4	673	4	US-10-063-589-16	Sequence 16, Appl	369	3078.5	98.2	676	4	US-10-029-386-33083	Sequence 33083, A
297	3083.5	98.4	673	4	US-10-063-593-16	Sequence 16, Appl	370	2935	93.6	672	4	US-10-050-704-99	Sequence 99, Appl
298	3083.5	98.4	673	4	US-10-063-596-16	Sequence 16, Appl	371	2935	93.6	672	4	US-10-798-512-99	Sequence 99, Appl
299	3083.5	98.4	673	4	US-10-063-600-16	Sequence 16, Appl	372	2935	93.6	723	4	US-10-050-704-186	Sequence 186, App
300	3083.5	98.4	673	4	US-10-063-604-16	Sequence 16, Appl	373	2935	93.6	723	4	US-10-798-512-186	Sequence 186, App
301	3083.5	98.4	673	4	US-10-063-612-16	Sequence 16, Appl	374	2490	79.4	673	3	US-09-782-980-68	Sequence 68, Appl
302	3083.5	98.4	673	4	US-10-063-616-16	Sequence 16, Appl	375	2490	79.4	673	4	US-10-806-018-68	Sequence 68, Appl
303	3083.5	98.4	673	4	US-10-063-615-16	Sequence 16, Appl	376	2494	79.2	673	4	US-10-487-421-10	Sequence 10, Appl
304	3083.5	98.4	673	4	US-10-063-640-16	Sequence 16, Appl	377	1178.5	37.6	281	3	US-09-866-050A-648	Sequence 648, App
305	3083.5	98.4	673	4	US-10-063-642-16	Sequence 16, Appl	378	980.5	31.3	207	5	US-10-491-355-18	Sequence 18, Appl
306	3083.5	98.4	673	4	US-10-063-644-16	Sequence 16, Appl	379	360.5	11.5	635	5	US-10-363-374-8	Sequence 8, Appl
307	3083.5	98.4	673	4	US-10-063-649-16	Sequence 16, Appl	380	360.5	11.5	647	4	US-10-093-463-188	Sequence 188, App
308	3083.5	98.4	673	4	US-10-063-650-16	Sequence 16, Appl	381	357.5	11.4	778	4	US-10-093-463-192	Sequence 192, App
309	3083.5	98.4	673	4	US-10-063-652-16	Sequence 16, Appl	382	339	10.8	566	4	US-10-093-463-190	Sequence 190, App
310	3083.5	98.4	673	4	US-10-063-654-16	Sequence 16, Appl	383	338	10.8	551	3	US-09-897-214-8	Sequence 8, Appl
311	3083.5	98.4	673	4	US-10-063-659-16	Sequence 16, Appl	384	337	10.7	553	3	US-09-957-187-10	Sequence 10, Appl
312	3083.5	98.4	673	4	US-10-063-661-16	Sequence 16, Appl	385	337	10.7	653	6	US-11-058-709-10	Sequence 10, Appl
313	3083.5	98.4	673	4	US-10-063-528-16	Sequence 16, Appl	386	333	10.6	590	3	US-09-957-187-12	Sequence 12, Appl
314	3083.5	98.4	673	4	US-10-063-540-16	Sequence 16, Appl	387	333	10.6	590	6	US-11-058-709-12	Sequence 12, Appl
315	3083.5	98.4	673	4	US-10-063-568-16	Sequence 16, Appl	388	332	10.6	526	5	US-10-450-763-35186	Sequence 35186, A
316	3083.5	98.4	673	4	US-10-063-570-16	Sequence 16, Appl	389	330	10.5	653	3	US-09-989-722-229	Sequence 229, App
317	3083.5	98.4	673	4	US-10-063-582-16	Sequence 16, Appl	390	330	10.5	653	3	US-09-989-723-229	Sequence 229, App
318	3083.5	98.4	673	4	US-10-063-587-16	Sequence 16, Appl	391	330	10.5	653	3	US-09-989-729-229	Sequence 229, App
319	3083.5	98.4	673	4	US-10-063-592-16	Sequence 16, Appl	392	330	10.5	653	3	US-09-989-727-229	Sequence 229, App



393	330	10.5	653	3	US-09-989-731-229	Sequence 229, App	466	330	10.5	653	4	US-10-176-918-438	Sequence 438, App
394	330	10.5	653	3	US-09-989-732-229	Sequence 229, App	467	330	10.5	653	4	US-10-176-921-438	Sequence 438, App
395	330	10.5	653	3	US-09-991-073-229	Sequence 229, App	468	330	10.5	653	4	US-10-137-865-438	Sequence 438, App
396	330	10.5	653	3	US-09-990-442-229	Sequence 229, App	469	330	10.5	653	4	US-10-140-474-438	Sequence 438, App
397	330	10.5	653	3	US-09-991-163-229	Sequence 229, App	470	330	10.5	653	4	US-10-142-431-438	Sequence 438, App
398	330	10.5	653	3	US-09-993-604-229	Sequence 229, App	471	330	10.5	653	4	US-10-143-114-438	Sequence 438, App
399	330	10.5	653	3	US-09-990-456-229	Sequence 229, App	472	330	10.5	653	4	US-10-142-419-438	Sequence 438, App
400	330	10.5	653	3	US-09-989-721-229	Sequence 229, App	473	330	10.5	653	4	US-10-123-262-438	Sequence 438, App
401	330	10.5	653	3	US-09-992-598-229	Sequence 229, App	474	330	10.5	653	4	US-10-142-423-438	Sequence 438, App
402	330	10.5	653	3	US-09-989-293A-229	Sequence 229, App	475	330	10.5	653	4	US-10-121-050-438	Sequence 438, App
403	330	10.5	653	3	US-09-989-735-229	Sequence 229, App	476	330	10.5	653	4	US-10-141-755-438	Sequence 438, App
404	330	10.5	653	3	US-09-990-444-229	Sequence 229, App	477	330	10.5	653	4	US-10-143-032-438	Sequence 438, App
405	330	10.5	653	3	US-09-991-181-229	Sequence 229, App	478	330	10.5	653	4	US-10-123-108-438	Sequence 438, App
406	330	10.5	653	3	US-09-989-730-229	Sequence 229, App	479	330	10.5	653	4	US-10-123-236-438	Sequence 438, App
407	330	10.5	653	3	US-09-990-436-229	Sequence 229, App	480	330	10.5	653	4	US-10-123-261-438	Sequence 438, App
408	330	10.5	653	3	US-09-993-687-229	Sequence 229, App	481	330	10.5	653	4	US-10-140-921-438	Sequence 438, App
409	330	10.5	653	3	US-09-989-734-229	Sequence 229, App	482	330	10.5	653	4	US-10-140-928-438	Sequence 438, App
410	330	10.5	653	3	US-09-997-653-229	Sequence 229, App	483	330	10.5	653	4	US-10-121-045-438	Sequence 438, App
411	330	10.5	653	3	US-09-997-428-229	Sequence 229, App	484	330	10.5	653	4	US-10-123-292-438	Sequence 438, App
412	330	10.5	653	3	US-09-989-724-229	Sequence 229, App	485	330	10.5	653	4	US-10-123-903-438	Sequence 438, App
413	330	10.5	653	3	US-09-989-728-229	Sequence 229, App	486	330	10.5	653	4	US-10-124-819-438	Sequence 438, App
414	330	10.5	653	3	US-09-990-441-229	Sequence 229, App	487	330	10.5	653	4	US-10-124-822-438	Sequence 438, App
415	330	10.5	653	3	US-09-993-667-229	Sequence 229, App	488	330	10.5	653	4	US-10-140-925-438	Sequence 438, App
416	330	10.5	653	3	US-09-997-428-229	Sequence 229, App	489	330	10.5	653	4	US-10-160-498-438	Sequence 438, App
417	330	10.5	653	3	US-09-997-666-229	Sequence 229, App	490	330	10.5	653	4	US-10-124-824-438	Sequence 438, App
418	330	10.5	653	3	US-09-990-562-229	Sequence 229, App	491	330	10.5	653	4	US-10-127-825A-438	Sequence 438, App
419	330	10.5	653	3	US-09-997-514-229	Sequence 229, App	492	330	10.5	653	4	US-10-127-829A-438	Sequence 438, App
420	330	10.5	653	3	US-09-991-172-229	Sequence 229, App	493	330	10.5	653	4	US-10-127-835A-438	Sequence 438, App
421	330	10.5	653	3	US-09-998-156-229	Sequence 229, App	494	330	10.5	653	4	US-10-127-839A-438	Sequence 438, App
422	330	10.5	653	3	US-09-990-437-229	Sequence 229, App	495	330	10.5	653	4	US-10-127-901A-438	Sequence 438, App
423	330	10.5	653	3	US-09-991-157-229	Sequence 229, App	496	330	10.5	653	4	US-10-128-693A-438	Sequence 438, App
424	330	10.5	653	3	US-09-997-573-229	Sequence 229, App	497	330	10.5	653	4	US-10-131-813A-438	Sequence 438, App
425	330	10.5	653	3	US-09-997-573-229	Sequence 229, App	498	330	10.5	653	4	US-10-131-818A-438	Sequence 438, App
426	330	10.5	653	3	US-09-991-172-229	Sequence 229, App	499	330	10.5	653	4	US-10-131-824A-438	Sequence 438, App
427	330	10.5	653	3	US-09-990-726-229	Sequence 229, App	500	330	10.5	653	4	US-10-131-824A-438	Sequence 438, App
428	330	10.5	653	3	US-09-997-559-229	Sequence 229, App	501	330	10.5	653	4	US-10-131-830A-438	Sequence 438, App
429	330	10.5	653	3	US-09-997-601-229	Sequence 229, App	502	330	10.5	653	4	US-10-131-837A-438	Sequence 438, App
430	330	10.5	653	3	US-09-990-443-229	Sequence 229, App	503	330	10.5	653	4	US-10-137-872A-438	Sequence 438, App
431	330	10.5	653	3	US-09-991-854-229	Sequence 229, App	504	330	10.5	653	4	US-10-147-500-438	Sequence 438, App
432	330	10.5	653	3	US-09-997-628-229	Sequence 229, App	505	330	10.5	653	4	US-10-147-502-438	Sequence 438, App
433	330	10.5	653	3	US-09-997-683-229	Sequence 229, App	506	330	10.5	653	4	US-10-147-515-438	Sequence 438, App
434	330	10.5	653	3	US-09-989-729A-229	Sequence 229, App	507	330	10.5	653	4	US-10-147-517-438	Sequence 438, App
435	330	10.5	653	3	US-09-997-349-229	Sequence 229, App	508	330	10.5	653	4	US-10-147-526-438	Sequence 438, App
436	330	10.5	653	3	US-09-997-440-229	Sequence 229, App	509	330	10.5	653	4	US-10-147-527-438	Sequence 438, App
437	330	10.5	653	3	US-09-990-440-229	Sequence 229, App	510	330	10.5	653	4	US-10-121-041-438	Sequence 438, App
438	330	10.5	653	3	US-09-997-857-229	Sequence 229, App	511	330	10.5	653	4	US-10-121-043-438	Sequence 438, App
439	330	10.5	653	3	US-09-993-469-229	Sequence 229, App	512	330	10.5	653	4	US-10-121-047-438	Sequence 438, App
440	330	10.5	653	3	US-09-997-542-229	Sequence 229, App	513	330	10.5	653	4	US-10-123-215-438	Sequence 438, App
441	330	10.5	653	3	US-09-993-748-229	Sequence 229, App	514	330	10.5	653	4	US-10-123-902-438	Sequence 438, App
442	330	10.5	653	3	US-09-990-439-229	Sequence 229, App	515	330	10.5	653	4	US-10-123-908-438	Sequence 438, App
443	330	10.5	653	3	US-09-990-427-229	Sequence 229, App	516	330	10.5	653	4	US-10-123-909-438	Sequence 438, App
444	330	10.5	653	3	US-09-989-328-229	Sequence 229, App	517	330	10.5	653	4	US-10-123-910-438	Sequence 438, App
445	330	10.5	653	3	US-09-993-583-229	Sequence 229, App	518	330	10.5	653	4	US-10-124-813-438	Sequence 438, App
446	330	10.5	653	3	US-09-941-992-229	Sequence 229, App	519	330	10.5	653	4	US-10-124-817-438	Sequence 438, App
447	330	10.5	653	3	US-09-992-521-229	Sequence 229, App	520	330	10.5	653	4	US-10-125-922-438	Sequence 438, App
448	330	10.5	653	3	US-09-997-333-229	Sequence 229, App	521	330	10.5	653	4	US-10-125-924-438	Sequence 438, App
449	330	10.5	653	3	US-09-997-384-229	Sequence 229, App	522	330	10.5	653	4	US-10-140-860-438	Sequence 438, App
450	330	10.5	653	3	US-09-998-041-229	Sequence 229, App	523	330	10.5	653	4	US-10-142-417-438	Sequence 438, App
451	330	10.5	653	3	US-09-997-585-229	Sequence 229, App	524	330	10.5	653	4	US-10-147-519-438	Sequence 438, App
452	330	10.5	653	3	US-09-997-614-229	Sequence 229, App	525	330	10.5	653	4	US-10-157-782-438	Sequence 438, App
453	330	10.5	653	3	US-09-989-862-229	Sequence 229, App	526	330	10.5	653	4	US-10-152-395-438	Sequence 438, App
454	330	10.5	653	3	US-09-997-529-229	Sequence 229, App	527	330	10.5	653	4	US-10-125-926A-438	Sequence 438, App
455	330	10.5	653	3	US-09-989-725-229	Sequence 229, App	528	330	10.5	653	4	US-10-125-930A-438	Sequence 438, App
456	330	10.5	653	3	US-09-991-150-229	Sequence 229, App	529	330	10.5	653	4	US-10-127-831A-438	Sequence 438, App
457	330	10.5	653	3	US-09-997-641-229	Sequence 229, App	530	330	10.5	653	4	US-10-127-837A-438	Sequence 438, App
458	330	10.5	653	3	US-09-989-733-229	Sequence 229, App	531	330	10.5	653	4	US-10-127-838B-438	Sequence 438, App
459	330	10.5	653	3	US-09-992-643-229	Sequence 229, App	532	330	10.5	653	4	US-10-127-842A-438	Sequence 438, App
460	330	10.5	653	4	US-10-028-072-438	Sequence 438, App	533	330	10.5	653	4	US-10-127-843A-438	Sequence 438, App
461	330	10.5	653	4	US-10-140-808-438	Sequence 438, App	534	330	10.5	653	4	US-10-127-845A-438	Sequence 438, App
462	330	10.5	653	4	US-10-121-049-438	Sequence 438, App	535	330	10.5	653	4	US-10-127-846A-438	Sequence 438, App
463	330	10.5	653	4	US-10-123-904-438	Sequence 438, App	536	330	10.5	653	4	US-10-127-848A-438	Sequence 438, App
464	330	10.5	653	4	US-10-140-470-438	Sequence 438, App	537	330	10.5	653	4	US-10-127-849A-438	Sequence 438, App
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892	330	10.5	653	4	US-10-142-426-438	Sequence 438, App	965	328.5	10.5	627	4	US-10-244-968-100	Sequence 100, App
893	330	10.5	653	4	US-10-140-024-438	Sequence 438, App	966	328.5	10.5	627	4	US-10-244-990-100	Sequence 100, App
894	330	10.5	653	4	US-10-147-536-438	Sequence 438, App	967	328.5	10.5	627	4	US-10-245-079-100	Sequence 100, App
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979	328.5	10.5	627	4	US-10-245-454-100	Sequence 100, App	1052	321	10.2	628	6	US-11-147-047-45	Sequence 45, Appl
980	328.5	10.5	627	4	US-10-237-471-100	Sequence 100, App	1053	321	10.2	762	4	US-10-489-988-2	Sequence 2, Appl
981	328.5	10.5	627	4	US-10-238-261-100	Sequence 100, App	1054	321	10.2	797	4	US-10-424-233-16	Sequence 16, Appl
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983	328.5	10.5	627	4	US-10-241-860-100	Sequence 100, App	1056	320	10.2	660	3	US-09-909-088B-28	Sequence 28, Appl
984	328.5	10.5	627	4	US-10-242-172-100	Sequence 100, App	1057	320	10.2	660	3	US-09-905-291A-28	Sequence 28, Appl
985	328.5	10.5	627	4	US-10-242-652-100	Sequence 100, App	1058	320	10.2	660	3	US-09-902-853-28	Sequence 28, Appl
986	328.5	10.5	627	4	US-10-242-990-100	Sequence 100, App	1059	320	10.2	660	3	US-09-907-824-28	Sequence 28, Appl
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988	328.5	10.5	627	4	US-10-243-103-100	Sequence 100, App	1061	320	10.2	660	3	US-09-904-011-28	Sequence 28, Appl
989	328.5	10.5	627	4	US-10-243-276-100	Sequence 100, App	1062	320	10.2	660	3	US-09-903-640-28	Sequence 28, Appl
990	328.5	10.5	627	4	US-10-243-326-100	Sequence 100, App	1063	320	10.2	660	3	US-09-908-093-28	Sequence 28, Appl
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996	328.5	10.5	627	4	US-10-245-479-100	Sequence 100, App	1069	320	10.2	660	3	US-09-909-204-28	Sequence 28, Appl
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998	328.5	10.5	627	4	US-10-245-772-100	Sequence 100, App	1071	320	10.2	660	3	US-09-904-786-28	Sequence 28, Appl
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ALIGNMENTS

RESULT 1

US-09-866-028-69

Sequence 69, Application US/09866028

Patent No. US20020058309A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Botstein, David

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Hillan, Kenneth

APPLICANT: Kljavin, Ivar

APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P2548P1C1

CURRENT APPLICATION NUMBER: US/09/866, 028

CURRENT FILING DATE: 2001-05-25

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 69

LENGTH: 598

TYPE: PRT

ORGANISM: Homo Sapien

US-09-866-028-69

Query Match 100.0%; Score 3135; DB 3; Length 598;

Best Local Similarity 100.0%; Pred. No. 2.4e-194;

Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ENGIMLDASSPAGLPGLQLDLSNQIASLRPLRLDLLSHNSLLALEPGLDITANVE 120

DB 61 ENGIMLDASSPAGLPGLQLDLSNQIASLRPLRLDLLSHNSLLALEPGLDITANVE 120

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QY 181 RPEDLAGLAALQELDVSNLSLOALPGDSLGLFPRLRLAAARNPNCVCLSMFGPWRE 240

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QY 541 GPAGAPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGLQSPHLHAKPYI 598  
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RESULT 2

US-09-944-449-69  
; Sequence 69, Application US/09944449  
; Patent No. US20020102647A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,449  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017

; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. US20020102647A1ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 69  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-944-449-69  
  
Query Match 100.0%; Score 3135; DB 3; Length 598;  
Best Local Similarity 100.0%; Pred No. 2 4e-194;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MCSRVPLLLPLLLLLALGPGVQCPSGQCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60  
Db 1 MCSRVPLLLPLLLLLALGPGVQCPSGQCQSQPQTVFCTARQGTTPRDPVPPDTVGLYVF 60  
  
QY 61 ENGITMLDASSFAGLPGQLQLLDLSQNIASRLPRLLLLDLSHNSLLALEPGLDITANVE 120  
Db 61 ENGITMLDASSFAGLPGQLQLLDLSQNIASRLPRLLLLDLSHNSLLALEPGLDITANVE 120  
  
QY 121 ALRLAGLGLQQLDEGLFSLRLNLDLDVSDNQLRPPVPIRGLRGLTRLRAGNTRIAQL 180











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; ORGANISM: Homo Sapien
US-09-944-862-69

Query Match      100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLLALGFGVGCPCGCGCQSQPQTVECTARQGTTPVRDVPDPTVGLYVF 60
DB 1 MCSRVPLLLPLLLLLALGFGVGCPCGCGCQSQPQTVECTARQGTTPVRDVPDPTVGLYVF 60

QY 61 ENGITWLDASSFAGLGLQLLDLSQNCIASLRLPRILLDDLSHNSLLALEPGLDITANVE 120
DB 61 ENGITWLDASSFAGLGLQLLDLSQNCIASLRLPRILLDDLSHNSLLALEPGLDITANVE 120

QY 121 ALRLAGLGLQQLDEGLFSRLNLHLDVSDNQLERVPVIRGLRGLTRLRLAGNTRIAQL 180
DB 121 ALRLAGLGLQQLDEGLFSRLNLHLDVSDNQLERVPVIRGLRGLTRLRLAGNTRIAQL 180

QY 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFCVCLSNWFGPWVRE 240
DB 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFCVCLSNWFGPWVRE 240

QY 241 SHVTLASPESTRCHFPKKNAGRLLLLELDYADFCCPATTATVPTTRPVVRBPTALSSSL 300
DB 241 SHVTLASPESTRCHFPKKNAGRLLLLELDYADFCCPATTATVPTTRPVVRBPTALSSSL 300

QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVPODCCPSTCLNGTCHLGRHHLACLCPG 360
DB 301 APTWLSPTAPATEAPSPSTAPPTVGPVPODCCPSTCLNGTCHLGRHHLACLCPG 360

QY 361 FTGLYCESQMGQCTRPSPPTVTPRPRSLTLGIEPVSPSLRVGLQRYLQSSVQLRSRLR 420
DB 361 FTGLYCESQMGQCTRPSPPTVTPRPRSLTLGIEPVSPSLRVGLQRYLQSSVQLRSRLR 420

QY 421 LTYRNLSGDPKRLVTLRLPASLAETVTOIRPNATYSVCVMPGLGPRVPEGEACEAHT 480
DB 421 LTYRNLSGDPKRLVTLRLPASLAETVTOIRPNATYSVCVMPGLGPRVPEGEACEAHT 480

QY 481 PPAVSHNHAPVTOAREGNPLLIAPALAAVLAALAAVGAACVRRGRAMAAADKGOV 540
DB 481 PPAVSHNHAPVTOAREGNPLLIAPALAAVLAALAAVGAACVRRGRAMAAADKGOV 540

QY 541 GFGAGPLELEGVKVPLEPGPKATEGGEALPGSCECEVPLMGFPGLQSPPLHAKPYI 598
DB 541 GFGAGPLELEGVKVPLEPGPKATEGGEALPGSCECEVPLMGFPGLQSPPLHAKPYI 598

RESULT 5
US-09-945-587-69
; Sequence 69, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Nary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
;
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020127643A1, September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020127643A1, September 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
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; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-69

Query Match      100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLLLALGPGVGCPCGSCOCSPQTVCTARQTTVPDRVDPDTVGLYVF 60
DB 1 MCSRVPLLLPLLLLLALGPGVGCPCGSCOCSPQTVCTARQTTVPDRVDPDTVGLYVF 60
QY 61 ENGITMLDASSFAGLPGQLQLDLDSQNIASRLRLPRLLLLDLSHNSLLALEPGILDPTANVE 120
DB 61 ENGITMLDASSFAGLPGQLQLDLDSQNIASRLRLPRLLLLDLSHNSLLALEPGILDPTANVE 120
QY 121 ALRLAGLQQLDEGLFSRLRNHLDDVSDNQLERVPPVIRGLRGLTRLRAGNTRIAQL 180
DB 121 ALRLAGLQQLDEGLFSRLRNHLDDVSDNQLERVPPVIRGLRGLTRLRAGNTRIAQL 180
QY 181 RPEDLAGLAALQELDVSNLSLQALPGDLGLFPRLLRLAAARNPFCVPLSFGFWVRE 240
DB 181 RPEDLAGLAALQELDVSNLSLQALPGDLGLFPRLLRLAAARNPFCVPLSFGFWVRE 240
QY 241 SHVTLASPESTRCHFFPKNAGRLLELDYADFQCPATTTTATVPTTRPVVREPTALSSSL 300
DB 241 SHVTLASPESTRCHFFPKNAGRLLELDYADFQCPATTTTATVPTTRPVVREPTALSSSL 300
QY 301 APTWLSPTAPATAPSPPTAPTVGVPOQPCPSTCLNGTCHLGRHHLACLCPEG 360
DB 301 APTWLSPTAPATAPSPPTAPTVGVPOQPCPSTCLNGTCHLGRHHLACLCPEG 360
QY 361 FTGLYCESQMGQTRSPSTVTPRPRSLTLGTIEPVSTSLRVGLQRYLQSSSVQLRSRLR 420
DB 361 FTGLYCESQMGQTRSPSTVTPRPRSLTLGTIEPVSTSLRVGLQRYLQSSSVQLRSRLR 420
QY 421 LTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATYSVCVMPILGPGRVPEGEACGEAHT 480
DB 421 LTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATYSVCVMPILGPGRVPEGEACGEAHT 480
QY 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKGV 540
DB 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGMAAAQDKGV 540
QY 541 GPAGAPLELGVKVPLEPPGPKATGGGALPGSGCECEVPLMGFPGLQSPFLHAKPYI 598
DB 541 GPAGAPLELGVKVPLEPPGPKATGGGALPGSGCECEVPLMGFPGLQSPFLHAKPYI 598

RESULT 6
US-09-945-015-69
; Sequence 69, Application US/09945015
; Patent No. US20020132768A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
```

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; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,015
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
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; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-015-69

Query Match 100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVP LLLP LLL L L A L G P V G C P S G C O C S Q P O T V F C T A R O G T T V P R D V P D T V G L Y V F 60
Db 1 MCSRVP LLLP LLL L L L L L L A L G P V G C P S G C O C S Q P O T V F C T A R O G T T V P R D V P D T V G L Y V F 60

QY 61 ENGITM D A S S F A G L P G L Q L L D L S Q N I A S L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E 120
Db 61 ENGITM D A S S F A G L P G L Q L L D L S Q N I A S L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E 120

QY 121 A L R L A G L Q Q L D E G L F S R L N L H D L D V S D N Q L E R V P P V I R G L R T R L R L A G N T R I A Q L 180
Db 121 A L R L A G L Q Q L D E G L F S R L N L H D L D V S D N Q L E R V P P V I R G L R T R L R L A G N T R I A Q L 180

QY 181 R P E D L A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W R E 240
Db 181 R P E D L A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W R E 240

QY 241 S H V T L A S P E T R C H P P K N A G R L L L E D Y A D F G C P A T T T T A T V T T P R P V V R E P T A L S S S L 300
Db 241 S H V T L A S P E T R C H P P K N A G R L L L E D Y A D F G C P A T T T T A T V T T P R P V V R E P T A L S S S L 300

QY 301 A P T W L S P T A P A T E A S P P S T A P T V G P V P Q D C P P S T C L N G T C H L G T R H L A C L C P E G 360
Db 301 A P T W L S P T A P A T E A S P P S T A P T V G P V P Q D C P P S T C L N G T C H L G T R H L A C L C P E G 360

QY 361 F T G L Y C E S Q M G G T R P S P T P T P R P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R 420
Db 361 F T G L Y C E S Q M G G T R P S P T P T P R P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R 420

QY 421 L T Y R N L S G P D K R L V T L R L P A S L A E Y T V T Q L R P N A T Y S V C M P L G P R V P E G E A C G E A H T 480
Db 421 L T Y R N L S G P D K R L V T L R L P A S L A E Y T V T Q L R P N A T Y S V C M P L G P R V P E G E A C G E A H T 480

QY 481 P P A V H S N H A P V T Q A R E G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G V 540
Db 481 P P A V H S N H A P V T Q A R E G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G V 540

QY 541 G P G A G P L E G V K V P L E P G P K A T E G G E A L P S G S E C E V P L M G F P P G C L O S P L H A K P Y I 598
Db 541 G P G A G P L E G V K V P L E P G P K A T E G G E A L P S G S E C E V P L M G F P P G C L O S P L H A K P Y I 598

RESULT 7

US-09-944-396-69
; Sequence 69, Application US/09944396
; Patent No. US20020132981A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/944,396
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
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; PRIOR APPLICATION NUMBER: 60/069,702
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; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
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; PRIOR FILING DATE: June 22, 1999
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; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020132981A1ember 30, 1999



; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
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; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-396-69

Query Match 100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCSRVPLLLPLLLALGPGVQCPCGQCQSQPTVCTARQTTVPRDVPDVTGLYVF 60
Db 1 MCSRVPLLLPLLLALGPGVQCPCGQCQSQPTVCTARQTTVPRDVPDVTGLYVF 60

QY 61 ENGITMLDASSFAGLPGQLDLSQNOIASRLPRLLLDLSHNSLLALEPGILDTANVE 120
Db 61 ENGITMLDASSFAGLPGQLDLSQNOIASRLPRLLLDLSHNSLLALEPGILDTANVE 120

QY 121 ALRLAGLGLQOLDEGLFSRLRNHLDVSDNQLERVPVIRGILTRLRACNTRIAQL 180
Db 121 ALRLAGLGLQOLDEGLFSRLRNHLDVSDNQLERVPVIRGILTRLRACNTRIAQL 180

QY 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLLLAARPNFNCVPLSWFGPWVRE 240
Db 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLLLAARPNFNCVPLSWFGPWVRE 240

QY 241 SHVTLASPEETRCHFPKXNAGRLLELDYADFCGPATTTTATVTPTRPVVREPTALSSSL 300
Db 241 SHVTLASPEETRCHFPKXNAGRLLELDYADFCGPATTTTATVTPTRPVVREPTALSSSL 300

QY 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTCHLGRHHLACLCPEG 360
Db 301 APTWLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTCHLGRHHLACLCPEG 360

QY 361 FTGLYCSQMGQTRPSPTVTPRPSRLTIGIEPVSPVSLRVLQRYLQSSVQLRSLR 420
Db 361 FTGLYCSQMGQTRPSPTVTPRPSRLTIGIEPVSPVSLRVLQRYLQSSVQLRSLR 420

QY 421 LTVRNLSGDPKRLVTLRLPLASLAETVTVQLRPNATYSCVMPGLGPRVPEGEACGGAHT 480
Db 421 LTVRNLSGDPKRLVTLRLPLASLAETVTVQLRPNATYSCVMPGLGPRVPEGEACGGAHT 480

QY 481 PPAVHSHNAPVTQAREGNLPLLIAPALAAVLAALAAVGAAYCVRRCRAMAAAAQDKGV 540
Db 481 PPAVHSHNAPVTQAREGNLPLLIAPALAAVLAALAAVGAAYCVRRCRAMAAAAQDKGV 540

QY 541 GPGAGPLEGKVKVPLFPGPKATGEGGALPSGSECEVPLMGFPGLQSPPLHAKPYI 598
Db 541 GPGAGPLEGKVKVPLFPGPKATGEGGALPSGSECEVPLMGFPGLQSPPLHAKPYI 598

US-09-944-432-69
; Sequence 69, Application US/09944432
; Patent No. US20020142419A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,432
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999



;; PRIOR APPLICATION NUMBER: PCT/US99/12252  
;; PRIOR FILING DATE: June 22, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: September 15, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28409  
;; PRIOR FILING DATE: No. US20020142419A1ember 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: No. US20020142419A1ember 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28301  
;; PRIOR FILING DATE: December 1, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: December 16, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US00/03565  
;; PRIOR FILING DATE: February 11, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
;; PRIOR FILING DATE: February 22, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/05841  
;; PRIOR FILING DATE: March 2, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/08439  
;; PRIOR FILING DATE: March 30, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/14042  
;; PRIOR FILING DATE: May 22, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/20710  
;; PRIOR FILING DATE: July 28, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: December 1, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US01/06520  
;; PRIOR FILING DATE: February 28, 2001  
;; NUMBER OF SEQ ID NOS: 120  
;; SEQ ID NO 69  
;; LENGTH: 598  
;; TYPE: PRT  
;; ORGANISM: Homo Sapien  
US-09-944-432-69

Query Match 100.0%; Score 3135; DB 3; Length 598;  
Best Local Similarity 100.0%; Pred. No. 2.4e-194; Indels 0; Gaps 0;  
Matches 598; Conservative 0; Mismatches 0;

QY 1 MCSRVPLLLPLLLLLALGFGVGCSPGSCQSPQVCTAROGTTVPDRVPPDTVGLYVF 60  
DB 1 MCSRVPLLLPLLLLLALGFGVGCSPGSCQSPQVCTAROGTTVPDRVPPDTVGLYVF 60  
QY 61 ENGITWLDASSPAGLPGLQLDLSONQIASLRPLRLLLDLSHNSLLALEPGILDTANVE 120  
DB 61 ENGITWLDASSPAGLPGLQLDLSONQIASLRPLRLLLDLSHNSLLALEPGILDTANVE 120  
QY 121 ALRLAGLGIQQLDEGLFSLRLNLDLDVSDNQLERVPVIRGLRGLTRLRAGNTRIAQL 180  
DB 121 ALRLAGLGIQQLDEGLFSLRLNLDLDVSDNQLERVPVIRGLRGLTRLRAGNTRIAQL 180  
QY 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLLAAARNPNCVCLSWFGPWVRE 240  
DB 181 RPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLLAAARNPNCVCLSWFGPWVRE 240  
QY 241 SHVTLASPEETKCHPPKKNAGRLLELDYADGCPATTTTATVTPRVPVREPTALSSSL 300  
DB 241 SHVTLASPEETKCHPPKKNAGRLLELDYADGCPATTTTATVTPRVPVREPTALSSSL 300  
QY 301 APTWLSPTAPATEAPSPSTAPPTGVPVPOQDCPPSTCLNGCTGCHLGRHHLACLCEPG 360  
DB 301 APTWLSPTAPATEAPSPSTAPPTGVPVPOQDCPPSTCLNGCTGCHLGRHHLACLCEPG 360  
QY 361 FTGLYCESOMGGTTPSPPTVTPRPSRLTLGIEPVSPSTSLRVGLQRYLQSSVOLRSRL 420  
DB 361 FTGLYCESOMGGTTPSPPTVTPRPSRLTLGIEPVSPSTSLRVGLQRYLQSSVOLRSRL 420  
QY 421 LTYRNLSPGDKRLVTLRLPASLAETVTLQLRPNATYSCVMPPLGRCVRPEGEACGEAHT 480  
DB 421 LTYRNLSPGDKRLVTLRLPASLAETVTLQLRPNATYSCVMPPLGRCVRPEGEACGEAHT 480  
QY 481 PPAVHSHNAPVTOAREGNLPLIIAPALAAVLAALAAVGAAYCVRGRGRAMAAAAQDKGV 540  
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Db 481 PPAVHSHNAPVTOAREGNLPLIIAPALAAVLAALAAVGAAYCVRGRGRAMAAAAQDKGV 540  
QY 541 GFGAGPLEGKVKVPLEPGPKATEGGGEALPGSGSECEVPLMGFPFGGLQSPHLHAKPYI 598  
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Db 541 GFGAGPLEGKVKVPLEPGPKATEGGGEALPGSGSECEVPLMGFPFGGLQSPHLHAKPYI 598  
|||||  
RESULT 9  
US-09-943-762-69  
;; Sequence 69, Application US/09943762  
;; Patent No. US20020142958A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Baker, Kevin  
;; APPLICANT: Botstein, David  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Gerritsen, Mary  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul  
;; APPLICANT: Grimaldi, Christopher  
;; APPLICANT: Gurney, Austin  
;; APPLICANT: Hillan, Kenneth  
;; APPLICANT: Kljavin, Ivar  
;; APPLICANT: Napier, Mary  
;; APPLICANT: Roy, Margaret  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Wood, William  
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE REFERENCE: P2548P1C1  
;; CURRENT APPLICATION NUMBER: US/09/943,762  
;; CURRENT FILING DATE: 2001-09-26  
;; PRIOR APPLICATION NUMBER: 09/866,028  
;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: 60/067,411  
;; PRIOR FILING DATE: December 3, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,334  
;; PRIOR FILING DATE: December 11, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,335  
;; PRIOR FILING DATE: December 11, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,278  
;; PRIOR FILING DATE: December 11, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,425  
;; PRIOR FILING DATE: December 12, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,696  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,694  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,702  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,870  
;; PRIOR FILING DATE: December 17, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,873  
;; PRIOR FILING DATE: December 17, 1997  
;; PRIOR APPLICATION NUMBER: 60/068,017  
;; PRIOR FILING DATE: December 18, 1997  
;; PRIOR APPLICATION NUMBER: 60/070,440  
;; PRIOR FILING DATE: January 5, 1998  
;; PRIOR APPLICATION NUMBER: 60/074,086  
;; PRIOR FILING DATE: February 9, 1998  
;; PRIOR APPLICATION NUMBER: 60/074,092  
;; PRIOR FILING DATE: February 9, 1998  
;; PRIOR APPLICATION NUMBER: 60/075,945  
;; PRIOR FILING DATE: February 25, 1998  
;; PRIOR APPLICATION NUMBER: 60/112,850  
;; PRIOR FILING DATE: December 16, 1998  
;; PRIOR APPLICATION NUMBER: 60/113,296  
;; PRIOR FILING DATE: December 22, 1998  
;; PRIOR APPLICATION NUMBER: 60/146,222  
;; PRIOR FILING DATE: July 28, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US98/19330  
;; PRIOR FILING DATE: September 16, 1998



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; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-943-762-69

Query Match      100.0%; Score 3135; DB 3; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MCSRVPLLLPLLLALLGPGVQCGPCGCGCQSQPQTVCFTARQGTTPRDVPPDPTVGLYVF 60
DB      1 MCSRVPLLLPLLLALLGPGVQCGPCGCGCQSQPQTVCFTARQGTTPRDVPPDPTVGLYVF 60
QY      61 ENGITWLDASSFAGLPGQLLDLSQNOIASRLPRLLILLDLSHNSLLALEPGLDITANVE 120
DB      61 ENGITWLDASSFAGLPGQLLDLSQNOIASRLPRLLILLDLSHNSLLALEPGLDITANVE 120
QY      121 ALRLAGLGLQDLGFLSRNLNHLDDVSNQLERVPPVIRGLRGLTRLAGNTRIAQL 180
DB      121 ALRLAGLGLQDLGFLSRNLNHLDDVSNQLERVPPVIRGLRGLTRLAGNTRIAQL 180
QY      181 RPEDLAGLAALQELDVSNLSQALPGDLSGLFRLRLLLAAARNPFCVCLSWFGPWVRE 240
DB      181 RPEDLAGLAALQELDVSNLSQALPGDLSGLFRLRLLLAAARNPFCVCLSWFGPWVRE 240
QY      241 SHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
DB      241 SHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
QY      301 APTWLSPTAPATEAPSPPTAPPTVGPVPOQDCCPSTCLNGGTCCHLGRHHLACLCPGEG 360
DB      301 APTWLSPTAPATEAPSPPTAPPTVGPVPOQDCCPSTCLNGGTCCHLGRHHLACLCPGEG 360
QY      361 FTGLYCSQMGQGTTPSPPTVTPRPSRLTIGIEPVSPTSLRVGLQRYLOGSSVQLRSRLR 420
DB      361 FTGLYCSQMGQGTTPSPPTVTPRPSRLTIGIEPVSPTSLRVGLQRYLOGSSVQLRSRLR 420
;
361 FTGLYCSQMGQGTTPSPPTVTPRPSRLTIGIEPVSPTSLRVGLQRYLOGSSVQLRSRLR 420
421 LTYRNLSPDKRLVTLRLPASLAETVTQLRPNATYSVCVMPPLGPRVPEGEACGEAHT 480
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541 GPGAGPLEGCVKVPLEBPGPKATEGGGEALPSGSECEVPLMGFPFGPGLQSPHLHAKPYI 598
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RESULT 10
US-09-944-654-69
; Sequence 69, Application US/09944654
; Patent No. US20020142959A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavich, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,654
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
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		PRIOR APPLICATION NUMBER:	60/112,850	
		PRIOR FILING DATE:	December 16, 1998	
		PRIOR APPLICATION NUMBER:	60/113,296	
		PRIOR FILING DATE:	December 22, 1998	
		PRIOR APPLICATION NUMBER:	60/146,222	
		PRIOR FILING DATE:	July 28, 1999	
		PRIOR APPLICATION NUMBER:	PCT/US98/19330	
		PRIOR FILING DATE:	September 16, 1998	
		PRIOR APPLICATION NUMBER:	PCT/US98/25108	
		PRIOR FILING DATE:	December 1, 1998	
		PRIOR APPLICATION NUMBER:	09/216,021	
		PRIOR FILING DATE:	December 16, 1998	
		PRIOR APPLICATION NUMBER:	09/218,517	
		PRIOR FILING DATE:	December 22, 1998	
		PRIOR APPLICATION NUMBER:	09/254,311	
		PRIOR FILING DATE:	March 3, 1999	
		PRIOR APPLICATION NUMBER:	PCT/US99/12252	
		PRIOR FILING DATE:	June 22, 1999	
		PRIOR APPLICATION NUMBER:	PCT/US99/21090	
		PRIOR FILING DATE:	September 15, 1999	
		PRIOR APPLICATION NUMBER:	PCT/US99/28409	
		PRIOR FILING DATE:	No. US20020142959A ember 30, 1999	
		PRIOR APPLICATION NUMBER:	PCT/US99/28313	
		PRIOR FILING DATE:	No. US20020142959A ember 30, 1999	
		PRIOR APPLICATION NUMBER:	PCT/US99/28301	
		PRIOR FILING DATE:	December 1, 1999	
		PRIOR APPLICATION NUMBER:	PCT/US99/30095	
		PRIOR FILING DATE:	December 16, 1999	
		PRIOR APPLICATION NUMBER:	PCT/US00/03565	
		PRIOR FILING DATE:	February 11, 2000	
		PRIOR APPLICATION NUMBER:	PCT/US00/04414	
		PRIOR FILING DATE:	February 22, 2000	
		PRIOR APPLICATION NUMBER:	PCT/US00/05841	
		PRIOR FILING DATE:	March 2, 2000	
		PRIOR APPLICATION NUMBER:	PCT/US00/08439	
		PRIOR FILING DATE:	March 30, 2000	
		PRIOR APPLICATION NUMBER:	PCT/US00/14042	
		PRIOR FILING DATE:	May 22, 2000	
		PRIOR APPLICATION NUMBER:	PCT/US00/20710	
		PRIOR FILING DATE:	July 28, 2000	
		PRIOR APPLICATION NUMBER:	PCT/US00/32678	
		PRIOR FILING DATE:	December 1, 2000	
		PRIOR APPLICATION NUMBER:	PCT/US01/06520	
		PRIOR FILING DATE:	February 28, 2001	
		NUMBER OF SEQ ID NOS:	120	
		SEQ ID NO	69	
		LENGTH:	598	
		TYPE:	PRT	
		ORGANISM:	Homo Sapien	
		US-09-944-654-69		
		Query Match	100.0%; Score 3135; DB 3;	Length 598;
		Best Local Similarity	100.0%; Pred.No.2.e-194;	
		Matches 598; Conservative	0; Mismatches	0; Indels 0; Gaps 0
Qy	1	MCSRVPLLLPLLLLALPGVGCGFCGSCQCQPQTVCFTARQGTTVPDRDPDTVGLYVF	60	
Dd	1	MCSRVPLLLPLLLLALPGVGCGFCGSCQCQPQTVCFTARQGTTVPDRDPDTVGLYVF	60	
Qy	61	ENGITMLDASSFAGLPGQLLDLSQNQTASLRPLRLDLLDSHNSLLALEPCILD TANVE	120	
Dd	61	ENGITMLDASSFAGLPGQLDLSDNQNTASLRPLRLDLLDSHNSLLALEPCILD TANVE	120	
Qy	121	ALRILAGLGLOQLDEGLFSRLRNHLHDVDSDNOLERVPPVRIGLTGLTRLLAGNTRIAQL	180	
Dd	121	ALRILAGLGLOQLDEGLFSRLRNHLHDVDSDNOLERVPPVRIGLTGLTRLLAGNTRIAQL	180	
Qy	181	RPEADLAGLAALQEIDVSNLSIQALFGDSLGLFPRLRLLLAAARNPNCCPSWFGPWVRE	240	
Dd	181	RPEADLAGLAALQEIDVSNLSIQALFGDSLGLFPRLRLLLAAARNPNCCPSWFGPWVRE	240	
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[illegible]



; PRIOR APPLICATION NUMBER: 60/069,702  
 ; PRIOR FILING DATE: December 16, 1997  
 ; PRIOR APPLICATION NUMBER: 60/069,870  
 ; PRIOR FILING DATE: December 17, 1997  
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 ; PRIOR FILING DATE: December 17, 1997  
 ; PRIOR APPLICATION NUMBER: 60/068,017  
 ; PRIOR FILING DATE: December 18, 1997  
 ; PRIOR APPLICATION NUMBER: 60/070,440  
 ; PRIOR FILING DATE: January 5, 1998  
 ; PRIOR APPLICATION NUMBER: 60/074,086  
 ; PRIOR FILING DATE: February 9, 1998  
 ; PRIOR APPLICATION NUMBER: 60/074,092  
 ; PRIOR FILING DATE: February 9, 1998  
 ; PRIOR APPLICATION NUMBER: 60/075,945  
 ; PRIOR FILING DATE: February 25, 1998  
 ; PRIOR APPLICATION NUMBER: 60/112,850  
 ; PRIOR FILING DATE: December 16, 1998  
 ; PRIOR APPLICATION NUMBER: 60/113,296  
 ; PRIOR FILING DATE: December 22, 1998  
 ; PRIOR APPLICATION NUMBER: 60/146,222  
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 ; PRIOR FILING DATE: September 16, 1998  
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108  
 ; PRIOR FILING DATE: December 1, 1998  
 ; PRIOR APPLICATION NUMBER: 09/216,021  
 ; PRIOR FILING DATE: December 16, 1998  
 ; PRIOR APPLICATION NUMBER: 09/218,517  
 ; PRIOR FILING DATE: December 22, 1998  
 ; PRIOR APPLICATION NUMBER: 09/254,311  
 ; PRIOR FILING DATE: March 3, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252  
 ; PRIOR FILING DATE: June 22, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: September 15, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409  
 ; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301  
 ; PRIOR FILING DATE: December 1, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: December 16, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565  
 ; PRIOR FILING DATE: February 11, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: February 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841  
 ; PRIOR FILING DATE: March 2, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439  
 ; PRIOR FILING DATE: March 30, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042  
 ; PRIOR FILING DATE: May 22, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710  
 ; PRIOR FILING DATE: July 28, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678  
 ; PRIOR FILING DATE: December 1, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520  
 ; PRIOR FILING DATE: February 28, 2001  
 ; NUMBER OF SEQ ID NOS: 120  
 ; SEQ ID NO 69  
 ; LENGTH: 598  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-09-944-413-69

Query Match 100.0%; Score 3135; DB 3; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;  
 Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 121 ALRLAGLGLQQLDEGLFSRLRLNLHDLVDSDNQLERVPVIRGLGLTRLRAGNTRIAOL 180  
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 Db 541 GPGAGPLEGKVKVPLEPGPKATEGGGALPGSGSECEVPLMGFPGGLQSPHLHAKPYI 598  
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RESULT 13

US-09-944-403-69  
 ; Sequence 69, Application US/09944403  
 ; Patent No. US20020165143A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul  
 ; APPLICANT: Grimaldi, Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Hillan, Kenneth  
 ; APPLICANT: Kljavin, Ivar  
 ; APPLICANT: Napier, Mary  
 ; APPLICANT: Roy, Margaret  
 ; APPLICANT: Tamas, Daniel  
 ; APPLICANT: Wood, William  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P2548P1C1  
 ; CURRENT APPLICATION NUMBER: US/09/944, 403  
 ; CURRENT FILING DATE: 2001-09-26  
 ; PRIOR APPLICATION NUMBER: 09/866, 028  
 ; PRIOR FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: 60/067,411  
 ; PRIOR FILING DATE: December 3, 1997  
 ; PRIOR APPLICATION NUMBER: 60/069,334  
 ; PRIOR FILING DATE: December 11, 1997  
 ; PRIOR APPLICATION NUMBER: 60/069,335  
 ; PRIOR FILING DATE: December 11, 1997



; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 69  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-09-944-403-69

Query Match 100.0%; Score 3135; DB 3; Length 598;  
Best Local Similarity 100.0%; Pred. No. 2.4e-194;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 MCSRVPLLLPLLLLLALGPGVCGCGSCQCPOTVCTARQGTTPVPRDVPDDTVGLVVF 60  
  
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Db 61 ENGITMLDASSFAGLPGQLQLDLDSQNOIASRLRLPRLLLDLSHNSLLALEPILDTANVE 120  
  
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Db 121 ALRLAGLQQLDEGLFSRLNLHDLVSDNQLERVPVIRGLRGLTLRLAGNTRIAQL 180  
  
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Db 191 RPEDLAGLAALQELDVSNLSIQALPGDLSGLFPRLRLAAARNPNCVPSWFGPWVRE 240  
  
QY 241 SHVTLASPEETRCHFPKPNAGRLLELDYADFGPCATTTTATVTPTRPVVREPTALSSSL 300  
Db 241 SHVTLASPEETRCHFPKPNAGRLLELDYADFGPCATTTTATVTPTRPVVREPTALSSSL 300  
  
QY 301 APTWLSPTAPATEAPSPSTAPPVGPVPOQDPPSTCLNGCTCHLGRHHLACLCPG 360  
Db 301 APTWLSPTAPATEAPSPSTAPPVGPVPOQDPPSTCLNGCTCHLGRHHLACLCPG 360  
  
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Db 361 FTGLYCESQMGQGTPTPTVTPRPSRSLTGLIEPVSPSLRVGLQRYLQGSVQLRSLR 420  
  
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Db 481 PPAVHSHNAPVTQAREGNLPLLIAPALAAVLAALAAVGAAYCVRGRGRAMAAADKGOV 540  
  
QY 541 GPGAGPLELEGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPGLQSPHLHAKPYI 598  
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RESULT 14

; Sequence 69, Application US/09944896  
; Patent No. US20020168715A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerriksen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,896  
; CURRENT FILING DATE: 2001-08-31



; PRIOR APPLICATION NUMBER: 09/866,028  
 ; PRIOR FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: 60/069,334  
 ; PRIOR FILING DATE: December 11, 1997  
 ; PRIOR APPLICATION NUMBER: 60/069,335  
 ; PRIOR FILING DATE: December 11, 1997  
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 ; PRIOR APPLICATION NUMBER: 60/068,017  
 ; PRIOR FILING DATE: December 18, 1997  
 ; PRIOR APPLICATION NUMBER: 60/070,440  
 ; PRIOR FILING DATE: January 5, 1998  
 ; PRIOR APPLICATION NUMBER: 60/074,086  
 ; PRIOR FILING DATE: February 9, 1998  
 ; PRIOR APPLICATION NUMBER: 60/074,092  
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 ; PRIOR APPLICATION NUMBER: 60/112,850  
 ; PRIOR FILING DATE: December 16, 1998  
 ; PRIOR APPLICATION NUMBER: 60/113,296  
 ; PRIOR FILING DATE: December 22, 1998  
 ; PRIOR APPLICATION NUMBER: 60/146,222  
 ; PRIOR FILING DATE: July 28, 1999  
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 ; PRIOR FILING DATE: September 16, 1998  
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108  
 ; PRIOR FILING DATE: December 1, 1998  
 ; PRIOR APPLICATION NUMBER: 09/216,021  
 ; PRIOR FILING DATE: December 16, 1998  
 ; PRIOR APPLICATION NUMBER: 09/218,517  
 ; PRIOR FILING DATE: December 22, 1998  
 ; PRIOR APPLICATION NUMBER: 09/254,311  
 ; PRIOR FILING DATE: March 3, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252  
 ; PRIOR FILING DATE: June 22, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: September 15, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409  
 ; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301  
 ; PRIOR FILING DATE: December 1, 1999  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
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 ; PRIOR FILING DATE: May 22, 2000  
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 ; PRIOR FILING DATE: July 28, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678  
 ; PRIOR FILING DATE: December 1, 2000  
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520

; PRIOR FILING DATE: February 28, 2001  
 ; NUMBER OF SEQ ID NOS: 120  
 ; SEQ ID NO 69  
 ; LENGTH: 598  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-09-944-896-69  
  
 Query Match 100.0%; Score 3135; DB 3; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;  
 Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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 DB 1 MCSRVPLLLPILLLLALGCVGCGCGCCGCGCOPQTVCTAROGTTVPRDVPDVTGLYVF 60  
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 DB 301 APTWLSPTAPATEAPSPSTAPPTVGPVPPQDCPPSTCLNGGTCCHLGRHHLACLCEG 360  
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 ; Sequence 69, Application US/09944944  
 ; Patent No. US20020173463A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul  
 ; APPLICANT: Grimaldi, Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Hillan, Kenneth  
 ; APPLICANT: Kllavin, Ivar  
 ; APPLICANT: Napier, Mary  
 ; APPLICANT: Roy, Margaret  
 ; APPLICANT: Tumas, Daniel







GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: July 27, 2006, 12:07:03 ; Search time 33 Seconds  
(without alignments)  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications\_AA\_New:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3135	100.0	598	7	US-11-296-155-69 Sequence 69, Appl
3	3083.5	98.4	673	7	US-11-101-316-16 Sequence 16, Appl
4	3083.5	98.4	673	7	US-11-376-673-16 Sequence 16, Appl
5	322.5	10.3	811	6	US-10-505-928-32 Sequence 32, Appl
6	322.5	10.3	811	6	US-10-505-928-87 Sequence 32, Appl
7	316.5	10.1	713	7	US-11-030-653-26 Sequence 26, Appl
8	313.5	10.0	656	7	US-11-030-653-38 Sequence 38, Appl
9	312	10.0	592	6	US-10-486-020-19 Sequence 19, Appl
10	312	10.0	592	7	US-11-030-653-14 Sequence 14, Appl
11	309	9.9	649	6	US-10-196-749-384 Sequence 384, Appl
12	309	9.9	649	7	US-11-101-316-132 Sequence 132, Appl
13	309	9.9	649	7	US-11-376-673-132 Sequence 132, Appl
14	282.5	9.0	745	7	US-11-293-697-3826 Sequence 3826, Appl
15	258	8.2	1523	6	US-10-196-749-290 Sequence 290, Appl
16	258	8.2	1523	6	US-10-533-365-236 Sequence 236, Appl
17	237	7.6	370	7	US-11-293-697-3248 Sequence 3248, Appl
18	237	7.6	370	6	US-10-505-928-33 Sequence 33, Appl
19	230.5	7.4	544	7	US-11-257-581-1 Sequence 1, Appl
20	230.5	7.4	544	7	US-11-257-579-1 Sequence 1, Appl
21	227.5	7.3	719	7	US-11-293-697-3841 Sequence 3841, Appl
22	226.5	7.2	291	7	US-11-197-712-304 Sequence 304, Appl
23	226.5	7.2	544	7	US-11-257-581-3 Sequence 3, Appl
24	226.5	7.2	544	7	US-11-257-579-3 Sequence 3, Appl
25	226.5	7.2	557	6	US-10-196-749-326 Sequence 326, Appl

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291	7	US-11-197-712-309	6.9	217.5	28	Sequence 109, Appl
716	6	US-10-518-039-6	6.8	214.5	29	Sequence 6, Appl
812	6	US-10-518-039-6	6.8	214.5	30	Sequence 5, Appl
531	7	US-11-257-581-6	6.8	212	31	Sequence 6, Appl
531	7	US-11-257-579-6	6.8	212	32	Sequence 6, Appl
513	7	US-11-101-316-124	6.7	211	33	Sequence 124, Appl
513	7	US-11-376-673-124	6.7	211	34	Sequence 124, Appl
531	7	US-11-257-581-5	6.7	211	35	Sequence 5, Appl
531	7	US-11-257-579-5	6.7	211	36	Sequence 5, Appl
531	7	US-11-257-581-4	6.7	210	37	Sequence 4, Appl
531	7	US-11-257-579-4	6.7	210	38	Sequence 4, Appl
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616	6	US-10-196-749-158	6.3	197.5	41	Sequence 158, Appl
423	7	US-11-030-653-28	6.2	195.5	42	Sequence 28, Appl
545	7	US-11-030-653-6	6.2	193.5	43	Sequence 6, Appl
40	7	US-11-134-871-326	6.2	193	44	Sequence 326, Appl
301	7	US-11-257-581-9	6.0	189.5	45	Sequence 9, Appl
301	7	US-11-257-579-9	6.0	189.5	46	Sequence 9, Appl
467	7	US-11-030-653-36	5.9	185	47	Sequence 36, Appl
302	7	US-11-257-581-7	5.9	184	48	Sequence 7, Appl
302	7	US-11-257-579-7	5.9	184	49	Sequence 7, Appl
368	6	US-10-505-928-743	5.9	184	50	Sequence 743, Appl
379	7	US-11-296-092-2	5.8	182.5	51	Sequence 2, Appl
379	7	US-11-296-155-2	5.8	182.5	52	Sequence 2, Appl
290	7	US-11-257-581-10	5.7	179	53	Sequence 10, Appl
290	7	US-11-257-581-11	5.7	179	54	Sequence 11, Appl
290	7	US-11-257-581-12	5.7	179	55	Sequence 12, Appl
290	7	US-11-257-579-10	5.7	179	56	Sequence 10, Appl
290	7	US-11-257-579-11	5.7	179	57	Sequence 11, Appl
290	7	US-11-257-579-12	5.7	179	58	Sequence 12, Appl
302	7	US-11-257-581-8	5.7	179	59	Sequence 8, Appl
302	7	US-11-257-579-8	5.7	179	60	Sequence 8, Appl
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359	6	US-10-933-854-18	5.5	172.5	62	Sequence 18, Appl
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1036	6	US-10-539-228-160	5.4	169.5	65	Sequence 160, Appl
577	6	US-10-449-902-50526	5.4	168	66	Sequence 50526, A
794	6	US-10-449-902-37455	5.3	167	67	Sequence 37455, A
544	7	US-11-056-3558-45953	5.3	166.5	68	Sequence 45953, A
544	7	US-11-056-3558-49766	5.3	166.5	69	Sequence 49766, A
546	7	US-11-056-3558-45952	5.3	166.5	70	Sequence 45952, A
546	7	US-11-056-3558-49765	5.3	166.5	71	Sequence 49765, A
549	7	US-11-056-3558-45951	5.3	166.5	72	Sequence 45951, A
549	7	US-11-056-3558-49764	5.3	166.5	73	Sequence 49764, A
32	7	US-11-134-871-3225	5.3	166	74	Sequence 3225, Appl
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515	7	US-11-056-3558-93502	5.3	165.5	76	Sequence 93502, A
521	7	US-11-056-3558-89745	5.3	165.5	77	Sequence 89745, A
521	7	US-11-056-3558-93501	5.3	165.5	78	Sequence 93501, A
526	7	US-11-056-3558-89744	5.3	165.5	79	Sequence 89744, A
526	7	US-11-056-3558-93500	5.3	165.5	80	Sequence 93500, A
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570	6	US-10-449-902-36779	5.2	164	82	Sequence 36779, A
611	6	US-10-520-783-2	5.2	164	83	Sequence 2, Appl
703	7	US-11-291-140-4	5.2	164	84	Sequence 4, Appl
904	7	US-11-144-322-2	5.2	164	85	Sequence 2, Appl
904	7	US-11-291-140-2	5.2	164	86	Sequence 2, Appl
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639	7	US-11-056-3558-69825	5.2	163.5	88	Sequence 69825, A
674	7	US-11-056-3558-69824	5.2	163.5	89	Sequence 69824, A
674	7	US-11-056-3558-75179	5.2	163.5	90	Sequence 75179, A
765	7	US-11-056-3558-75178	5.2	163.5	91	Sequence 75178, A
786	7	US-11-056-3558-69823	5.2	163.5	92	Sequence 69823, A
826	7	US-11-056-3558-75177	5.2	163.5	93	Sequence 75177, A
501	6	US-10-449-902-48020	5.2	163	94	Sequence 48020, A
599	7	US-11-056-3558-91592	5.1	160	95	Sequence 91592, A
599	7	US-11-056-3558-95348	5.1	160	96	Sequence 95348, A
634	7	US-11-056-3558-91591	5.1	160	97	Sequence 91591, A
634	7	US-11-056-3558-95347	5.1	160	98	Sequence 95347, A



99	160	5.1	744	7	US-11-056-355B-91590	Sequence 91590, A	172	147	4.7	2414	7	US-11-283-329-176	Sequence 176, App
100	160	5.1	744	7	US-11-056-355B-93346	Sequence 95346, A	173	146.5	4.7	925	7	US-11-056-355B-70331	Sequence 70331, A
101	159.5	5.1	494	7	US-11-056-355B-97011	Sequence 97011, A	174	146	4.7	293	6	US-10-953-348-22365	Sequence 22365, A
102	159	5.1	396	6	US-10-449-902-43379	Sequence 43379, A	175	146	4.7	748	6	US-10-953-348-3827	Sequence 3827, Ap
103	159	5.1	543	6	US-10-449-902-55599	Sequence 55599, A	176	146	4.7	785	6	US-10-953-349-8326	Sequence 8326, Ap
104	158.5	5.1	912	7	US-11-056-355B-87717	Sequence 87717, A	177	146	4.7	885	6	US-10-505-928-432	Sequence 432, App
105	158.5	5.1	993	7	US-11-056-355B-87716	Sequence 87716, A	178	146	4.7	785	7	US-11-251-465-20	Sequence 20, Appl
106	158.5	5.1	1070	7	US-11-056-355B-87715	Sequence 87715, A	179	146	4.7	978	6	US-10-953-349-9199	Sequence 9199, Ap
107	158	5.0	363	7	US-11-174-307B-4510	Sequence 4510, Ap	180	146	4.7	1173	6	US-10-953-349-9198	Sequence 9198, Ap
108	157.5	5.0	1032	6	US-10-196-749-552	Sequence 552, App	181	145.5	4.6	352	6	US-10-449-902-32358	Sequence 32358, A
109	157	5.0	1032	7	US-11-341-319-3	Sequence 3, Appli	182	145.5	4.6	352	6	US-10-449-902-32813	Sequence 32813, A
110	156.5	5.0	551	6	US-10-449-902-36375	Sequence 36375, A	183	145.5	4.6	352	6	US-10-449-902-44462	Sequence 44462, A
111	156.5	5.0	932	7	US-11-056-355B-87907	Sequence 87907, A	184	145.5	4.6	827	6	US-10-449-902-54991	Sequence 54991, A
112	156.5	5.0	932	7	US-11-056-355B-97149	Sequence 97149, A	185	145.5	4.6	1189	6	US-10-540-844-4	Sequence 4, Appli
113	156.5	5.0	965	7	US-11-056-355B-97148	Sequence 97148, A	186	145.5	4.6	1236	6	US-10-540-844-2	Sequence 2, Appli
114	156.5	5.0	980	7	US-11-056-355B-87906	Sequence 87906, A	187	145	4.6	292	7	US-11-056-355B-15849	Sequence 15849, A
115	156.5	5.0	980	7	US-11-056-355B-879147	Sequence 879147, A	188	145	4.6	338	7	US-11-105-233-144	Sequence 144, App
116	156.5	5.0	995	7	US-11-056-355B-87905	Sequence 87905, A	189	145	4.6	458	7	US-11-056-355B-56389	Sequence 56389, A
117	155.5	5.0	700	6	US-10-511-795-2	Sequence 2, Appli	190	145	4.6	518	7	US-11-056-355B-56388	Sequence 56388, A
118	155	4.9	411	6	US-10-953-349-33758	Sequence 33758, A	191	145	4.6	540	7	US-11-056-355B-56387	Sequence 56387, A
119	155	4.9	411	7	US-11-056-355B-7403	Sequence 7403, Ap	192	145	4.6	553	7	US-11-056-355B-15848	Sequence 15848, A
120	155	4.9	411	7	US-11-056-355B-19209	Sequence 19209, A	193	145	4.6	971	6	US-11-056-355B-15848	Sequence 52625, A
121	155	4.9	412	6	US-10-953-349-33757	Sequence 33757, A	194	145	4.6	1032	7	US-11-341-319-2	Sequence 2, Appli
122	155	4.9	412	7	US-11-056-355B-7402	Sequence 7402, Ap	195	144.5	4.6	692	6	US-10-196-749-560	Sequence 560, App
123	155	4.9	412	7	US-11-056-355B-19208	Sequence 19208, A	196	144.5	4.6	906	6	US-10-511-795-4	Sequence 4, Appli
124	155	4.9	581	6	US-10-449-902-55557	Sequence 55557, A	197	144	4.6	1072	6	US-10-449-902-53937	Sequence 53937, A
125	154.5	4.9	514	7	US-11-174-307B-4386	Sequence 4386, Ap	198	143.5	4.6	431	7	US-11-056-355B-106706	Sequence 106706, A
126	154.5	4.9	1192	7	US-11-056-355B-46297	Sequence 46297, A	199	143.5	4.6	431	7	US-11-056-355B-117945	Sequence 117945, A
127	154.5	4.9	2517	7	US-11-283-329-204	Sequence 204, App	200	143.5	4.6	450	7	US-11-056-355B-106705	Sequence 106705, A
128	154	4.9	461	6	US-10-953-349-24311	Sequence 24311, A	201	143.5	4.6	450	7	US-11-056-355B-117944	Sequence 117944, A
129	154	4.9	461	7	US-11-056-355B-53536	Sequence 52536, A	202	143.5	4.6	496	7	US-11-056-355B-106704	Sequence 106704, A
130	154	4.9	492	6	US-10-953-349-24310	Sequence 24310, A	203	143.5	4.6	603	7	US-11-056-355B-88145	Sequence 88145, A
131	154	4.9	492	7	US-11-056-355B-52535	Sequence 52535, A	204	143.5	4.6	605	7	US-11-056-355B-79474	Sequence 79474, A
132	154	4.9	1010	7	US-11-056-355B-78678	Sequence 78678, A	206	143.5	4.6	605	7	US-11-056-355B-88144	Sequence 88144, A
133	154	4.9	1090	7	US-11-056-355B-78677	Sequence 78677, A	207	143.5	4.6	611	7	US-11-056-355B-79473	Sequence 79473, A
134	153.5	4.9	775	7	US-11-056-355B-88930	Sequence 88930, A	208	143.5	4.6	613	7	US-11-056-355B-79472	Sequence 79472, A
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138	153.5	4.9	1032	7	US-11-341-319-1	Sequence 1, Appli	212	141.5	4.5	1335	6	US-10-449-902-41294	Sequence 41294, A
139	153.5	4.9	1041	7	US-11-056-355B-96010	Sequence 96010, A	213	141.5	4.5	460	7	US-11-056-355B-46185	Sequence 46185, A
140	153.5	4.9	1121	6	US-10-449-902-52117	Sequence 52117, A	214	141.5	4.5	460	7	US-11-056-355B-46184	Sequence 46184, A
141	153.5	4.9	1121	6	US-10-449-902-53982	Sequence 53982, A	215	141.5	4.5	475	7	US-11-056-355B-46183	Sequence 46183, A
142	152	4.8	682	6	US-10-449-902-53729	Sequence 53729, A	216	141.5	4.5	1052	6	US-10-449-902-46489	Sequence 46489, A
143	152	4.8	682	6	US-10-449-902-55720	Sequence 55720, A	217	140.5	4.5	1084	6	US-10-449-902-52915	Sequence 52915, A
144	152	4.8	776	7	US-11-056-355B-69962	Sequence 69962, A	218	140.5	4.5	533	6	US-10-953-349-10988	Sequence 10988, A
145	151	4.8	470	6	US-10-449-902-43319	Sequence 43319, A	219	140.5	4.5	656	6	US-10-449-902-38110	Sequence 38110, A
146	150.5	4.8	1061	6	US-10-449-902-48173	Sequence 48173, A	220	140.5	4.5	757	7	US-11-226-554-134	Sequence 134, App
147	150.5	4.8	1109	7	US-11-330-403-3817	Sequence 3817, Ap	221	140.5	4.5	757	7	US-11-226-554-135	Sequence 135, App
148	150.5	4.8	1109	7	US-11-330-403-9397	Sequence 9397, Ap	222	140.5	4.5	757	7	US-11-248-718-134	Sequence 134, App
149	150	4.8	367	7	US-11-105-233-62	Sequence 62, Appl	223	140.5	4.5	757	7	US-11-248-718-135	Sequence 135, App
150	149.5	4.8	848	6	US-10-449-902-41026	Sequence 41026, A	224	140.5	4.5	953	7	US-11-056-355B-107904	Sequence 107904, A
151	149	4.8	308	6	US-10-449-902-36640	Sequence 36640, A	225	140.5	4.5	953	7	US-11-056-355B-119143	Sequence 119143, A
152	149	4.8	419	6	US-10-449-902-38614	Sequence 38614, A	226	140.5	4.5	953	7	US-11-056-355B-46620	Sequence 46620, A
153	149	4.8	444	7	US-11-056-355B-106189	Sequence 106189, A	227	140.5	4.5	998	7	US-11-056-355B-46619	Sequence 46619, A
154	149	4.8	444	7	US-11-056-355B-117428	Sequence 117428, A	228	140.5	4.5	1009	7	US-11-056-355B-46618	Sequence 46618, A
155	149	4.8	471	7	US-11-056-355B-106188	Sequence 106188, A	229	140	4.5	1016	7	US-11-056-355B-69815	Sequence 69815, A
156	149	4.8	471	7	US-11-056-355B-117427	Sequence 117427, A	230	140	4.5	754	7	US-11-056-355B-81300	Sequence 81300, A
157	149	4.8	477	7	US-11-056-355B-106187	Sequence 106187, A	231	140	4.5	883	7	US-11-056-355B-81299	Sequence 81299, A
158	149	4.8	477	7	US-11-056-355B-117426	Sequence 117426, A	232	140	4.5	943	7	US-11-330-403-17817	Sequence 17817, A
159	149	4.8	1504	6	US-10-505-928-662	Sequence 662, App	233	140	4.5	999	7	US-11-056-355B-81298	Sequence 81298, A
160	148.5	4.7	511	6	US-10-449-902-44072	Sequence 44072, A	234	140	4.5	1029	7	US-11-056-355B-79833	Sequence 79833, A
161	147.5	4.7	386	7	US-11-056-355B-78532	Sequence 78532, A	235	139.5	4.4	2014	7	US-11-056-355B-79832	Sequence 79832, A
162	147.5	4.7	398	7	US-11-056-355B-78531	Sequence 78531, A	236	139.5	4.4	439	7	US-11-056-355B-79832	Sequence 79832, A
163	147.5	4.7	445	7	US-11-056-355B-89859	Sequence 89859, A	237	139.5	4.4	451	6	US-10-953-349-22994	Sequence 22994, A
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165	147.5	4.7	452	7	US-11-056-355B-78530	Sequence 78530, A	239	139.5	4.4	453	6	US-10-953-349-22993	Sequence 22993, A
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169	147.5	4.7	521	7	US-11-056-355B-93613	Sequence 93613, A	243	139.5	4.4	506	7	US-11-056-355B-79831	Sequence 79831, A
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171	147.5	4.7	964	6	US-10-449-902-47345	Sequence 47345, A							



245	139	4.4	5179	7	US-11-105-233-185	Sequence 185, App	318	128.5	4.1	697	6	US-10-953-349-3828	Sequence 3828, Ap
246	138.5	4.4	660	6	US-10-449-902-36212	Sequence 36212, A	319	128.5	4.1	744	7	US-11-056-3558-95855	Sequence 95855, A
247	138.5	4.4	811	6	US-10-196-749-414	Sequence 414, App	320	128.5	4.1	925	7	US-11-293-697-3889	Sequence 3889, Ap
248	138	4.4	675	6	US-10-449-902-48447	Sequence 48447, A	321	128.5	4.1	962	6	US-10-449-902-52324	Sequence 52324, A
249	138	4.4	675	6	US-10-449-902-50618	Sequence 50618, A	322	128.5	4.1	985	7	US-11-056-3558-988230	Sequence 88230, A
250	137	4.4	207	7	US-11-174-3078-5004	Sequence 5004, Ap	323	128.5	4.1	985	7	US-11-056-3558-91986	Sequence 91986, A
251	137	4.4	412	7	US-11-056-3558-15925	Sequence 15925, A	324	128.5	4.1	1460	7	US-11-247-437-14	Sequence 14, Appl
252	137	4.4	973	6	US-10-449-902-45886	Sequence 45886, A	325	128	4.1	213	7	US-11-056-3558-1607	Sequence 1607, Ap
253	137	4.4	1059	6	US-10-449-902-56147	Sequence 56147, A	326	128	4.1	213	7	US-11-056-3558-8787	Sequence 8787, Ap
254	136.5	4.4	161	6	US-10-449-902-54204	Sequence 54204, A	327	128	4.1	280	7	US-11-056-3558-1606	Sequence 1606, Ap
255	136.5	4.4	535	6	US-10-449-902-41243	Sequence 41243, A	328	128	4.1	367	7	US-11-056-3558-8785	Sequence 8785, Ap
256	136	4.3	322	7	US-11-246-999-79	Sequence 79, Appl	329	128	4.1	998	7	US-11-330-403-13360	Sequence 13360, A
257	136	4.3	586	6	US-10-449-902-51689	Sequence 51689, A	330	128	4.1	1115	6	US-10-449-902-55146	Sequence 55146, A
258	135.5	4.3	406	6	US-10-953-349-31643	Sequence 31643, A	331	128	4.1	1145	7	US-11-330-403-7343	Sequence 7343, Ap
259	135.5	4.3	406	7	US-11-056-3558-68135	Sequence 68135, A	332	127.5	4.1	428	7	US-11-056-3558-2964	Sequence 2964, Ap
260	135.5	4.3	440	7	US-11-251-465-65	Sequence 65, Appl	333	127.5	4.1	544	7	US-11-056-3558-2962	Sequence 2962, Ap
261	135.5	4.3	464	7	US-11-056-3558-91633	Sequence 91633, A	334	127.5	4.1	628	7	US-11-056-3558-69963	Sequence 69963, A
262	135.5	4.3	464	7	US-11-056-3558-95389	Sequence 95389, A	335	127.5	4.1	749	7	US-11-293-697-4038	Sequence 4038, Ap
263	135.5	4.3	493	7	US-11-056-3558-91632	Sequence 91632, A	336	127.5	4.1	750	7	US-11-056-3558-46834	Sequence 46834, A
264	135.5	4.3	493	7	US-11-056-3558-95388	Sequence 95388, A	337	127.5	4.1	750	7	US-11-056-3558-91032	Sequence 91032, A
265	135.5	4.3	998	7	US-11-330-403-13357	Sequence 13357, A	338	127.5	4.1	750	7	US-11-056-3558-94788	Sequence 94788, A
266	135.5	4.3	1012	6	US-10-953-349-13624	Sequence 13624, A	339	127.5	4.1	768	7	US-11-056-3558-46833	Sequence 46833, A
267	135.5	4.3	1025	6	US-10-953-349-13623	Sequence 13623, A	340	127.5	4.1	768	7	US-11-056-3558-91031	Sequence 91031, A
268	134.5	4.3	812	7	US-11-056-3558-96011	Sequence 96011, A	341	127.5	4.1	768	7	US-11-056-3558-94787	Sequence 94787, A
269	134.5	4.3	847	7	US-11-056-3558-79588	Sequence 79588, A	342	127.5	4.1	860	7	US-11-056-3558-46832	Sequence 46832, A
270	134.5	4.3	2240	6	US-10-544-731-4	Sequence 4, Appl	343	127.5	4.1	860	7	US-11-056-3558-91030	Sequence 91030, A
271	134.5	4.3	2258	6	US-10-544-731-3	Sequence 3, Appl	344	127.5	4.1	860	7	US-11-056-3558-94786	Sequence 94786, A
272	134.5	4.3	2264	6	US-10-544-731-5	Sequence 5, Appl	345	127.5	4.1	905	7	US-11-056-3558-46299	Sequence 46299, A
273	134	4.3	476	7	US-11-056-3558-41016	Sequence 16525, A	346	127.5	4.1	948	7	US-11-056-3558-83031	Sequence 83031, A
274	134	4.3	502	7	US-11-174-3078-5262	Sequence 5262, Ap	347	127.5	4.1	1000	7	US-11-056-3558-46298	Sequence 46298, A
275	134	4.3	697	6	US-10-449-902-50662	Sequence 50662, A	348	127.5	4.1	1010	7	US-11-056-3558-83030	Sequence 83030, A
276	134	4.3	921	6	US-10-519-135-6	Sequence 6, Appl	349	127.5	4.1	1120	7	US-11-056-3558-83029	Sequence 83029, A
277	133.5	4.3	239	7	US-11-293-697-2474	Sequence 2474, Ap	350	127	4.1	773	7	US-11-056-3558-97107	Sequence 97107, A
278	133.5	4.3	239	7	US-11-293-697-2850	Sequence 2850, Ap	351	127	4.1	1073	6	US-10-713-648A-54	Sequence 54, Appl
279	133.5	4.3	288	6	US-10-449-902-41012	Sequence 41012, A	352	127	4.1	1595	6	US-10-486-020-18	Sequence 18, Appl
280	133.5	4.3	744	6	US-10-449-902-41606	Sequence 41606, A	353	127	4.1	1614	7	US-11-056-3558-98827	Sequence 98827, A
281	133	4.2	694	7	US-11-056-3558-72373	Sequence 72373, A	354	127	4.1	1614	7	US-11-056-3558-32583	Sequence 32583, A
282	133	4.2	932	6	US-10-519-135-8	Sequence 8, Appl	355	127	4.1	1660	7	US-11-056-3558-88826	Sequence 88826, A
283	133	4.2	4391	6	US-11-183-325-56	Sequence 56, Appl	356	127	4.1	1660	7	US-11-056-3558-92582	Sequence 92582, A
284	132.5	4.2	332	7	US-11-246-999-32	Sequence 32, Appl	357	127	4.1	1828	7	US-11-056-3558-88825	Sequence 88825, A
285	132.5	4.2	587	7	US-11-030-653-32	Sequence 32, Appl	358	127	4.1	1828	7	US-11-056-3558-92581	Sequence 92581, A
286	132.5	4.2	691	7	US-11-056-3558-79590	Sequence 79590, A	359	127	4.1	1842	7	US-11-056-3558-82005	Sequence 82005, A
287	132.5	4.2	718	7	US-11-056-3558-79589	Sequence 79589, A	360	127	4.1	1850	7	US-11-056-3558-82004	Sequence 82004, A
288	132	4.2	717	7	US-11-056-3558-71164	Sequence 71164, A	361	127	4.1	1895	7	US-11-056-3558-50250	Sequence 50250, A
289	132	4.2	891	6	US-10-449-902-53978	Sequence 53978, A	362	126.5	4.0	262	7	US-10-196-749-110	Sequence 110, App
290	132	4.2	891	6	US-10-449-902-56281	Sequence 56281, A	363	126.5	4.0	438	6	US-10-449-902-56142	Sequence 56142, A
291	132	4.2	987	7	US-11-330-403-13361	Sequence 13361, A	364	126.5	4.0	638	6	US-10-449-902-56142	Sequence 56142, A
292	131	4.2	213	6	US-10-449-902-48867	Sequence 48867, A	365	126.5	4.0	685	7	US-11-175-714-2	Sequence 2, Appl
293	131	4.2	213	6	US-10-449-902-51210	Sequence 51210, A	366	126.5	4.0	685	7	US-11-175-714-28	Sequence 28, Appl
294	131	4.2	766	6	US-10-449-902-36778	Sequence 36778, A	367	126.5	4.0	685	7	US-11-175-714-32	Sequence 32, Appl
295	131	4.2	938	7	US-11-330-403-10157	Sequence 10157, A	368	126.5	4.0	685	7	US-11-175-714-34	Sequence 34, Appl
296	131	4.2	1074	6	US-10-449-902-52953	Sequence 52953, A	369	126.5	4.0	685	7	US-11-175-714-36	Sequence 36, Appl
297	130.5	4.2	177	7	US-11-056-3558-9410	Sequence 9410, Ap	370	126.5	4.0	685	7	US-11-175-714-38	Sequence 38, Appl
298	130.5	4.2	450	6	US-10-449-902-43069	Sequence 43069, A	371	126.5	4.0	685	7	US-11-178-724-20	Sequence 20, Appl
299	130.5	4.2	2003	7	US-11-264-243-8	Sequence 8, Appl	372	126.5	4.0	685	7	US-11-264-243-2	Sequence 2, Appl
300	130	4.1	296	7	US-11-056-3558-91655	Sequence 91655, A	373	126.5	4.0	685	7	US-11-071-796A-19	Sequence 19, Appl
301	130	4.1	296	7	US-11-056-3558-95411	Sequence 95411, A	374	126.5	4.0	718	6	US-10-449-902-53348	Sequence 53348, A
302	130	4.1	389	7	US-11-056-3558-91654	Sequence 91654, A	375	126.5	4.0	977	6	US-10-449-902-50081	Sequence 50081, A
303	130	4.1	389	7	US-11-056-3558-95410	Sequence 95410, A	376	126	4.0	670	7	US-11-056-3558-95856	Sequence 95856, A
304	130	4.1	693	7	US-11-293-697-3849	Sequence 3849, Ap	377	126	4.0	739	6	US-10-539-228-435	Sequence 425, App
305	130	4.1	915	6	US-10-523-014-4	Sequence 4, Appl	378	126	4.0	996	7	US-11-293-716-60	Sequence 60, Appl
306	129.5	4.1	806	7	US-11-056-3558-78679	Sequence 78679, A	379	126	4.0	1006	6	US-10-449-902-43074	Sequence 43074, A
307	129	4.1	652	6	US-10-953-349-5551	Sequence 5551, Ap	380	126	4.0	1786	6	US-10-519-328-2	Sequence 2, Appl
308	129	4.1	652	7	US-11-056-3558-30482	Sequence 30482, A	381	126	4.0	1821	6	US-10-505-928-451	Sequence 451, App
309	129	4.1	652	7	US-11-056-3558-34072	Sequence 34072, A	382	126	4.0	1821	6	US-10-519-328-1	Sequence 1, Appl
310	129	4.1	652	7	US-11-056-3558-97017	Sequence 97017, A	383	125.5	4.0	220	7	US-11-056-3558-50251	Sequence 50251, A
311	129	4.1	1040	7	US-11-056-3558-88229	Sequence 88229, A	384	125.5	4.0	258	6	US-10-196-749-284	Sequence 284, App
312	129	4.1	1040	7	US-11-056-3558-91985	Sequence 91985, A	385	125.5	4.0	508	6	US-10-449-902-30106	Sequence 30106, A
313	129	4.1	1126	7	US-11-293-697-3665	Sequence 3665, Ap	386	125.5	4.0	564	7	US-11-056-3558-38683	Sequence 38683, A
314	129	4.1	1210	7	US-11-056-3558-88228	Sequence 88228, A	387	125.5	4.0	577	7	US-11-056-3558-38682	Sequence 38682, A
315	129	4.1	1210	7	US-11-056-3558-91984	Sequence 91984, A	388	125.5	4.0	686	7	US-11-264-243-4	Sequence 4, Appl
316	129	4.1	2074	7	US-11-165-586-21	Sequence 21, Appl	389	125.5	4.0	944	7	US-11-056-3558-96336	Sequence 96336, A
317	128.5	4.1	671	6	US-10-449-902-52071	Sequence 52071, A	390	125.5	4.0	946	7	US-11-056-3558-96335	Sequence 96335, A



391	125.5	4.0	1003	7	US-11-056-355B-50497	Sequence 50497, A	464	122	3.9	1620	7	US-11-217-997-42	Sequence 42, Appl
392	125	4.0	293	6	US-10-953-349-31470	Sequence 31470, A	465	122	3.9	1653	7	US-11-217-997-40	Sequence 40, Appl
393	125	4.0	690	7	US-11-330-403-4347	Sequence 4347, Ap	466	122	3.9	2203	6	US-10-539-228-726	Sequence 726, App
394	125	4.0	706	6	US-10-449-902-44028	Sequence 44028, A	467	122	3.9	2511	7	US-11-051-725-12	Sequence 12, Appl
395	125	4.0	763	7	US-11-056-355B-107905	Sequence 107905,	468	122	3.9	2511	7	US-11-051-725-13	Sequence 13, Appl
396	125	4.0	763	7	US-11-056-355B-119144	Sequence 119144,	469	122	3.9	2523	7	US-11-051-725-11	Sequence 11, Appl
397	125	4.0	917	6	US-10-504-973-26	Sequence 26, Appl	470	121.5	3.9	294	7	US-11-056-355B-98134	Sequence 98134, A
398	125	4.0	2124	7	US-11-283-329-160	Sequence 160, App	471	121.5	3.9	294	7	US-11-056-355B-109373	Sequence 109373,
399	124.5	4.0	298	7	US-11-297-134-25	Sequence 25, Appl	472	121.5	3.9	296	7	US-11-056-355B-98133	Sequence 98133, A
400	124.5	4.0	546	6	US-10-196-749-412	Sequence 412, App	473	121.5	3.9	296	7	US-11-056-355B-109372	Sequence 109372,
401	124.5	4.0	884	6	US-10-449-902-53270	Sequence 53270, A	474	121.5	3.9	306	7	US-11-056-355B-84354	Sequence 84354, A
402	124.5	4.0	999	6	US-10-519-135-4	Sequence 4, Appli	475	121.5	3.9	314	7	US-11-056-355B-84353	Sequence 84353, A
403	124.5	4.0	1352	7	US-11-056-355B-44895	Sequence 44895, A	476	121.5	3.9	325	7	US-11-056-355B-40921	Sequence 40921, A
404	124.5	4.0	2556	7	US-11-264-243-6	Sequence 6, Appli	477	121.5	3.9	334	7	US-11-056-355B-91924	Sequence 91924, A
405	124	4.0	351	7	US-11-056-355B-65587	Sequence 65587, A	478	121.5	3.9	334	7	US-11-056-355B-95680	Sequence 95680, A
406	124	4.0	739	7	US-11-056-355B-79347	Sequence 79347, A	479	121.5	3.9	338	7	US-11-056-355B-88896	Sequence 88896, A
407	124	4.0	739	7	US-11-056-355B-84020	Sequence 84020, A	480	121.5	3.9	338	7	US-11-056-355B-92652	Sequence 92652, A
408	124	4.0	766	7	US-11-056-355B-79346	Sequence 79346, A	481	121.5	3.9	342	7	US-11-056-355B-40920	Sequence 40920, A
409	124	4.0	766	7	US-11-056-355B-84019	Sequence 84019, A	482	121.5	3.9	351	7	US-11-056-355B-91923	Sequence 91923, A
410	124	4.0	800	7	US-11-056-355B-84018	Sequence 84018, A	483	121.5	3.9	351	7	US-11-056-355B-95679	Sequence 95679, A
411	124	4.0	800	7	US-11-056-355B-91076	Sequence 91076, A	484	121.5	3.9	352	7	US-11-056-355B-95679	Sequence 95679, A
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413	124	4.0	839	6	US-10-449-902-49998	Sequence 49998, A	486	121.5	3.9	367	7	US-11-056-355B-98132	Sequence 98132, A
414	124	4.0	839	6	US-10-449-902-53600	Sequence 53600, A	487	121.5	3.9	367	7	US-11-056-355B-109371	Sequence 109371,
415	124	4.0	891	7	US-11-056-355B-91075	Sequence 91075, A	488	121.5	3.9	395	7	US-11-056-355B-47882	Sequence 47882, A
416	124	4.0	891	7	US-11-056-355B-94831	Sequence 94831, A	489	121.5	3.9	395	7	US-11-056-355B-88895	Sequence 88895, A
417	124	4.0	1011	7	US-11-056-355B-91074	Sequence 91074, A	490	121.5	3.9	395	7	US-11-056-355B-88895	Sequence 88895, A
418	124	4.0	1011	7	US-11-056-355B-94830	Sequence 94830, A	491	121.5	3.9	430	6	US-10-953-349-5789	Sequence 5789, Ap
419	124	4.0	1035	6	US-10-449-902-55142	Sequence 55142, A	492	121.5	3.9	430	7	US-11-056-355B-27332	Sequence 27332, A
420	124	4.0	2617	7	US-11-051-725-14	Sequence 14, Appl	493	121.5	3.9	430	7	US-11-056-355B-47881	Sequence 47881, A
421	123.5	3.9	324	6	US-10-449-902-34182	Sequence 34182, A	494	121.5	3.9	430	7	US-11-056-355B-88894	Sequence 88894, A
422	123.5	3.9	718	6	US-10-449-902-53222	Sequence 53222, A	495	121.5	3.9	430	7	US-11-056-355B-92650	Sequence 92650, A
423	123.5	3.9	898	7	US-11-056-355B-79052	Sequence 79052, A	496	121.5	3.9	432	6	US-10-953-349-5788	Sequence 5788, Ap
424	123.5	3.9	1002	6	US-10-449-902-45681	Sequence 45681, A	497	121.5	3.9	432	7	US-11-056-355B-27331	Sequence 27331, A
425	123.5	3.9	1140	6	US-10-449-902-41227	Sequence 41227, A	498	121.5	3.9	432	7	US-11-056-355B-47880	Sequence 47880, A
426	123.5	3.9	1198	7	US-11-217-997-14	Sequence 14, Appl	499	121.5	3.9	436	6	US-10-953-349-5787	Sequence 5787, Ap
427	123	3.9	411	6	US-10-953-349-16133	Sequence 16133, A	500	121.5	3.9	436	7	US-11-056-355B-27330	Sequence 27330, A
428	123	3.9	441	7	US-11-174-307B-5246	Sequence 5246, Ap	501	121.5	3.9	686	7	US-11-175-714-25	Sequence 25, Appl
429	123	3.9	458	6	US-10-953-349-16132	Sequence 16132, A	502	121.5	3.9	686	7	US-11-175-714-40	Sequence 40, Appl
430	123	3.9	477	6	US-10-953-349-16131	Sequence 16131, A	503	121.5	3.9	686	7	US-11-175-714-42	Sequence 42, Appl
431	123	3.9	618	7	US-11-178-724-19	Sequence 19, Appl	504	121.5	3.9	686	7	US-11-175-714-44	Sequence 44, Appl
432	123	3.9	618	7	US-11-071-796A-18	Sequence 18, Appl	505	121.5	3.9	686	7	US-11-175-714-46	Sequence 46, Appl
433	123	3.9	630	6	US-10-449-902-43648	Sequence 43648, A	506	121.5	3.9	760	7	US-11-056-355B-47907	Sequence 47907, A
434	122.5	3.9	329	6	US-10-953-349-8629	Sequence 8629, Ap	507	121.5	3.9	813	7	US-11-056-355B-37149	Sequence 37149, A
435	122.5	3.9	329	6	US-11-056-355B-42456	Sequence 42456, A	508	121.5	3.9	813	7	US-11-056-355B-37204	Sequence 37204, A
436	122.5	3.9	329	7	US-11-056-355B-106169	Sequence 106169,	509	121.5	3.9	851	7	US-11-056-355B-37148	Sequence 37148, A
437	122.5	3.9	329	7	US-11-056-355B-117408	Sequence 117408,	510	121.5	3.9	851	7	US-11-056-355B-37203	Sequence 37203, A
438	122.5	3.9	335	6	US-11-293-697-4002	Sequence 4002, Ap	511	121.5	3.9	863	7	US-11-289-102-215	Sequence 215, App
439	122.5	3.9	415	6	US-10-953-349-8628	Sequence 8628, Ap	512	121.5	3.9	863	7	US-11-289-102-264	Sequence 264, App
440	122.5	3.9	415	7	US-11-056-355B-42455	Sequence 42455, A	513	121.5	3.9	902	7	US-11-056-355B-37147	Sequence 37147, A
441	122.5	3.9	415	7	US-11-056-355B-106168	Sequence 106168,	514	121.5	3.9	902	7	US-11-056-355B-37202	Sequence 37202, A
442	122.5	3.9	415	7	US-11-056-355B-117407	Sequence 117407,	515	121.5	3.9	1332	6	US-10-449-902-41138	Sequence 41138, A
443	122.5	3.9	515	6	US-10-449-902-47898	Sequence 47898, A	516	121	3.9	294	7	US-11-051-725-71	Sequence 71, Appl
444	122.5	3.9	541	6	US-10-449-902-38744	Sequence 38744, A	517	121	3.9	294	7	US-11-051-725-72	Sequence 72, Appl
445	122.5	3.9	702	7	US-11-056-355B-85266	Sequence 85266, A	518	121	3.9	299	6	US-10-953-349-39478	Sequence 39478, A
446	122.5	3.9	848	6	US-10-539-228-371	Sequence 371, App	519	121	3.9	299	7	US-11-056-355B-13269	Sequence 13269, Ap
447	122.5	3.9	884	6	US-10-449-902-56049	Sequence 56049, A	520	121	3.9	522	6	US-10-449-902-44062	Sequence 44062, A
448	122.5	3.9	1036	7	US-11-248-956-2	Sequence 2, Appli	521	121	3.9	522	6	US-10-449-902-41167	Sequence 41167, A
449	122.5	3.9	1154	7	US-11-301-457-23	Sequence 23, Appl	522	121	3.9	2117	6	US-10-449-902-15081	Sequence 15081, A
450	122.5	3.9	22152	6	US-10-544-944-1	Sequence 35415, A	523	120.5	3.8	647	7	US-11-056-355B-46418	Sequence 46418, A
451	122	3.9	434	6	US-10-449-902-35415	Sequence 35415, A	524	120.5	3.8	647	7	US-11-056-355B-48177	Sequence 48177, A
452	122	3.9	434	6	US-10-449-902-36128	Sequence 36128, A	525	120.5	3.8	671	6	US-10-449-902-55560	Sequence 55560, A
453	122	3.9	495	7	US-11-174-307B-3112	Sequence 3112, Ap	526	120.5	3.8	695	7	US-11-056-355B-46417	Sequence 46417, A
454	122	3.9	575	7	US-11-217-997-32	Sequence 32, Appl	527	120.5	3.8	695	7	US-11-056-355B-48176	Sequence 48176, A
455	122	3.9	715	7	US-11-056-355B-85259	Sequence 85259, A	528	120.5	3.8	915	6	US-10-449-902-53511	Sequence 53511, A
456	122	3.9	718	7	US-11-056-355B-81584	Sequence 81584, A	529	120.5	3.8	949	6	US-10-953-349-12074	Sequence 12074, A
457	122	3.9	1398	7	US-11-217-997-4	Sequence 4, Appli	530	120.5	3.8	959	6	US-10-953-349-12073	Sequence 12073, A
458	122	3.9	1403	7	US-11-217-997-12	Sequence 12, Appl	531	120.5	3.8	966	6	US-10-519-135-10	Sequence 10, Appl
459	122	3.9	1404	7	US-11-217-997-2	Sequence 2, Appli	532	120.5	3.8	976	6	US-10-519-135-2	Sequence 2, Appli
460	122	3.9	1547	7	US-11-217-997-22	Sequence 22, Appl	533	120.5	3.8	976	7	US-11-056-355B-46416	Sequence 46416, A
461	122	3.9	1577	7	US-11-217-997-16	Sequence 16, Appl	534	120.5	3.8	976	7	US-11-056-355B-48175	Sequence 48175, A
462	122	3.9	1577	7	US-11-217-997-20	Sequence 20, Appl	535	120.5	3.8	1003	7	US-10-953-349-12072	Sequence 12072, A
463	122	3.9	1594	7	US-11-217-997-18	Sequence 18, Appl	536	120.5	3.8	1003	7	US-11-056-355B-48695	Sequence 48695, A



537	120.5	3.8	2503	6	US-10-539-228-723	Sequence 723, App	610	117	3.7	604	6	US-10-449-902-45317	Sequence 45317, A
538	120	3.8	243	7	US-11-056-355B-15926	Sequence 15926, A	611	117	3.7	655	7	US-11-242-617-1	Sequence 1, Appl
539	120	3.8	292	7	US-11-051-725-58	Sequence 58, Appl	612	117	3.7	681	6	US-10-953-349-10919	Sequence 10919, A
540	120	3.8	294	7	US-11-051-725-60	Sequence 60, Appl	613	117	3.7	681	7	US-11-056-355B-45477	Sequence 45477, A
541	120	3.8	294	7	US-11-051-725-80	Sequence 80, Appl	614	117	3.7	681	7	US-11-056-355B-49007	Sequence 49007, A
542	120	3.8	294	7	US-11-051-725-82	Sequence 82, Appl	615	117	3.7	698	6	US-10-449-902-53993	Sequence 53993, A
543	120	3.8	294	7	US-11-051-725-88	Sequence 88, Appl	616	117	3.7	727	6	US-10-449-902-38675	Sequence 38675, A
544	120	3.8	294	7	US-11-051-725-90	Sequence 90, Appl	617	117	3.7	988	7	US-11-056-355B-72321	Sequence 72321, A
545	120	3.8	332	6	US-10-449-902-32733	Sequence 32733, A	618	117	3.7	1238	7	US-11-178-724-22	Sequence 22, Appl
546	120	3.8	332	6	US-10-449-902-54788	Sequence 54788, A	619	117	3.7	1238	7	US-11-071-796A-21	Sequence 21, Appl
547	120	3.8	373	6	US-10-953-349-31149	Sequence 31149, A	620	117	3.7	1463	7	US-11-288-992-48	Sequence 48, Appl
548	120	3.8	546	7	US-11-056-355B-19161	Sequence 19161, A	621	117	3.7	2082	7	US-11-330-403-9531	Sequence 9531, Ap
549	120	3.8	560	6	US-10-449-902-53097	Sequence 53097, A	622	116.5	3.7	184	7	US-11-056-355B-30244	Sequence 30244, A
550	120	3.8	1047	6	US-10-449-902-53278	Sequence 53278, A	623	116.5	3.7	184	7	US-11-056-355B-33834	Sequence 33834, A
551	119.5	3.8	383	6	US-10-449-902-43496	Sequence 43496, A	624	116.5	3.7	710	6	US-10-449-902-53008	Sequence 53008, A
552	119.5	3.8	941	7	US-11-056-355B-72901	Sequence 72901, A	625	116.5	3.7	736	7	US-11-056-355B-107906	Sequence 107906, A
553	119.5	3.8	1031	6	US-10-449-902-52986	Sequence 52986, A	626	116.5	3.7	736	7	US-11-056-355B-119145	Sequence 119145, A
554	119.5	3.8	1104	7	US-11-056-355B-106433	Sequence 106433, A	627	116.5	3.7	942	7	US-11-056-355B-44897	Sequence 44897, A
555	119.5	3.8	1104	7	US-11-056-355B-117672	Sequence 117672, A	628	116.5	3.7	1081	7	US-11-056-355B-44896	Sequence 44896, A
556	119.5	3.8	1106	7	US-11-056-355B-106432	Sequence 106432, A	629	116	3.7	321	6	US-10-540-845-5	Sequence 5, Appl
557	119.5	3.8	1106	7	US-11-056-355B-117671	Sequence 117671, A	630	116	3.7	363	6	US-10-540-845-17	Sequence 17, Appl
558	119.5	3.8	1128	7	US-11-056-355B-106431	Sequence 106431, A	631	116	3.7	377	6	US-10-953-349-9913	Sequence 9913, Ap
559	119.5	3.8	1128	7	US-11-056-355B-117670	Sequence 117670, A	632	116	3.7	383	6	US-10-540-845-16	Sequence 16, Appl
560	119	3.8	272	6	US-10-953-349-3121	Sequence 3121, A	633	116	3.7	389	6	US-10-540-845-18	Sequence 18, Appl
561	119	3.8	406	6	US-10-449-902-42711	Sequence 42711, A	634	116	3.7	418	6	US-10-953-349-9912	Sequence 9912, Ap
562	119	3.8	554	6	US-10-449-902-46816	Sequence 46816, A	635	116	3.7	474	6	US-10-953-349-9911	Sequence 9911, Ap
563	119	3.8	598	6	US-10-953-349-8508	Sequence 8508, Ap	636	116	3.7	673	6	US-10-449-902-54153	Sequence 54153, A
564	119	3.8	598	7	US-11-056-355B-39871	Sequence 39871, A	637	116	3.7	680	6	US-10-449-902-47513	Sequence 47513, A
565	119	3.8	599	6	US-10-953-349-8507	Sequence 8507, Ap	638	116	3.7	1014	6	US-10-449-902-52994	Sequence 52994, A
566	119	3.8	599	7	US-11-056-355B-39870	Sequence 39870, A	639	116	3.7	1953	7	US-11-264-243-15	Sequence 16, Appl
567	119	3.8	627	7	US-11-056-355B-95163	Sequence 95163, A	640	116	3.7	2556	7	US-11-071-796A-22	Sequence 22, Appl
568	119	3.8	629	6	US-10-449-902-50256	Sequence 50256, A	641	116	3.7	3934	7	US-11-165-586-20	Sequence 20, Appl
569	119	3.8	695	6	US-10-449-902-48334	Sequence 48334, A	642	115.5	3.7	374	6	US-10-953-349-33957	Sequence 33957, A
570	119	3.8	737	7	US-11-056-355B-47908	Sequence 47908, A	643	115.5	3.7	375	7	US-11-056-355B-3621	Sequence 3621, Ap
571	119	3.8	750	7	US-11-056-355B-86395	Sequence 86395, A	644	115.5	3.7	396	7	US-11-056-355B-83842	Sequence 83842, A
572	119	3.8	751	7	US-11-056-355B-86395	Sequence 86395, A	645	115.5	3.7	822	7	US-11-056-355B-96337	Sequence 96337, A
573	119	3.8	751	7	US-11-296-444-47	Sequence 47, Appl	646	115.5	3.7	849	7	US-11-056-355B-79057	Sequence 79057, A
574	119	3.8	752	7	US-11-056-355B-91409	Sequence 91409, A	647	115.5	3.7	856	6	US-10-449-902-41385	Sequence 41385, A
575	119	3.8	752	7	US-11-056-355B-95165	Sequence 95165, A	648	115.5	3.7	911	7	US-11-226-554-89	Sequence 89, Appl
576	119	3.8	765	7	US-11-056-355B-91408	Sequence 91408, A	649	115.5	3.7	911	7	US-11-248-718-89	Sequence 89, Appl
577	119	3.8	765	7	US-11-056-355B-95164	Sequence 95164, A	650	115.5	3.7	970	7	US-11-056-355B-79056	Sequence 79056, A
578	119	3.8	809	7	US-11-056-355B-91407	Sequence 91407, A	651	115.5	3.7	1450	7	US-11-217-997-6	Sequence 6, Appl
579	119	3.8	809	6	US-10-505-928-150	Sequence 150, App	652	115	3.7	227	6	US-10-953-349-3122	Sequence 3122, A
580	119	3.8	5738	6	US-10-505-928-150	Sequence 150, App	653	115	3.7	337	7	US-11-174-307B-4220	Sequence 4220, Ap
581	118.5	3.8	248	6	US-10-953-349-20505	Sequence 20505, A	654	115	3.7	492	6	US-10-953-349-29544	Sequence 29544, A
582	118.5	3.8	373	7	US-11-056-355B-62373	Sequence 62373, A	655	115	3.7	492	6	US-11-056-355B-65692	Sequence 65692, A
583	118.5	3.8	890	7	US-11-056-355B-91072	Sequence 91072, A	656	115	3.7	679	7	US-11-056-355B-89082	Sequence 89082, A
584	118.5	3.8	890	7	US-11-056-355B-94828	Sequence 94828, A	657	115	3.7	679	7	US-11-056-355B-92838	Sequence 92838, A
585	118.5	3.8	895	7	US-11-056-355B-72905	Sequence 72905, A	658	115	3.7	680	7	US-11-056-355B-50712	Sequence 50712, A
586	118.5	3.8	998	7	US-11-056-355B-91071	Sequence 91071, A	659	115	3.7	740	6	US-10-449-902-53111	Sequence 53111, A
587	118.5	3.8	998	7	US-11-056-355B-94827	Sequence 94827, A	660	115	3.7	756	7	US-11-056-355B-89081	Sequence 89081, A
588	118.5	3.8	1010	7	US-11-056-355B-91070	Sequence 91070, A	661	115	3.7	756	7	US-11-056-355B-92837	Sequence 92837, A
589	118.5	3.8	1010	7	US-11-056-355B-94826	Sequence 94826, A	662	115	3.7	757	7	US-11-056-355B-50711	Sequence 50711, A
590	118.5	3.8	2245	7	US-11-248-956-3	Sequence 3, Appl	663	115	3.7	1375	6	US-10-553-436-181	Sequence 181, App
591	118	3.8	262	6	US-10-953-349-27149	Sequence 27149, A	664	114.5	3.7	297	6	US-10-953-349-31196	Sequence 31196, A
592	118	3.8	262	7	US-11-056-355B-63081	Sequence 63081, A	665	114.5	3.7	297	7	US-11-056-355B-66249	Sequence 66249, A
593	118	3.8	438	7	US-11-056-355B-7182	Sequence 7182, Ap	666	114.5	3.7	310	6	US-10-449-902-45786	Sequence 45786, A
594	118	3.8	493	7	US-11-056-355B-65494	Sequence 65494, A	667	114.5	3.7	330	7	US-11-056-355B-41942	Sequence 41942, A
595	118	3.8	1000	7	US-11-056-355B-46949	Sequence 46949, A	668	114.5	3.7	341	7	US-11-056-355B-72398	Sequence 72398, A
596	118	3.8	1031	7	US-11-056-355B-46948	Sequence 46948, A	669	114.5	3.7	368	7	US-11-056-355B-72397	Sequence 72397, A
597	118	3.8	1033	6	US-10-449-902-55424	Sequence 55424, A	670	114.5	3.7	373	7	US-11-056-355B-41941	Sequence 41941, A
598	118	3.8	1034	7	US-11-056-355B-46947	Sequence 46947, A	671	114.5	3.7	411	6	US-10-953-349-31856	Sequence 31856, A
599	118	3.8	1060	6	US-10-449-902-41453	Sequence 41453, A	672	114.5	3.7	411	7	US-11-056-355B-66649	Sequence 66649, A
600	118	3.8	2471	7	US-11-071-796A-23	Sequence 23, Appl	673	114.5	3.7	412	6	US-10-953-349-31855	Sequence 31855, A
601	117.5	3.7	369	6	US-10-449-902-50707	Sequence 50707, A	674	114.5	3.7	412	7	US-11-056-355B-66648	Sequence 66648, A
602	117.5	3.7	413	7	US-11-056-355B-4735	Sequence 4735, Ap	675	114.5	3.7	435	6	US-10-449-902-42063	Sequence 42063, A
603	117.5	3.7	550	7	US-11-056-355B-75616	Sequence 75616, A	676	114.5	3.7	451	6	US-10-953-349-31854	Sequence 31854, A
604	117.5	3.7	550	7	US-11-056-355B-96078	Sequence 96078, A	677	114.5	3.7	451	7	US-11-056-355B-66647	Sequence 66647, A
605	117.5	3.7	559	7	US-11-056-355B-87370	Sequence 87370, A	678	114.5	3.7	492	7	US-11-056-355B-10398	Sequence 10398, A
606	117.5	3.7	573	7	US-11-056-355B-75615	Sequence 75615, A	679	114.5	3.7	607	7	US-11-330-403-1414	Sequence 1414, Ap
607	117.5	3.7	582	7	US-11-056-355B-87369	Sequence 87369, A	680	114.5	3.7	688	7	US-11-330-403-5573	Sequence 5573, Ap
608	117.5	3.7	795	6	US-10-449-902-34693	Sequence 34693, A	681	114.5	3.7	910	7	US-11-056-355B-79291	Sequence 79291, A
609	117.5	3.7	870	6	US-10-539-228-358	Sequence 358, App	682	114.5	3.7	970	7	US-11-056-355B-79290	Sequence 79290, A



683	114.5	3.7	1046	7	US-11-056-355B-73289	Sequence 79289, A	756	112.5	3.6	142	7	US-11-056-355B-30245	Sequence 30245, A
684	114.5	3.7	1139	6	US-10-449-902-52733	Sequence 52733, A	757	112.5	3.6	142	7	US-11-056-355B-33835	Sequence 33835, A
685	114.5	3.7	1218	7	US-11-071-796A-20	Sequence 20, Appl	758	112.5	3.6	331	6	US-10-449-902-33293	Sequence 33293, A
686	114.5	3.7	1218	7	US-11-071-796A-20	Sequence 20, Appl	759	112.5	3.6	359	7	US-11-056-355B-83843	Sequence 83843, A
687	114.5	3.7	1360	7	US-11-330-403-4001	Sequence 4001, Ap	760	112.5	3.6	380	6	US-10-449-902-31350	Sequence 31350, A
688	114	3.6	177	6	US-10-953-349-34144	Sequence 34144, A	761	112.5	3.6	405	6	US-10-449-902-36521	Sequence 36521, A
689	114	3.6	184	7	US-11-293-697-2749	Sequence 2749, Ap	762	112.5	3.6	405	6	US-10-449-902-54849	Sequence 54849, A
690	114	3.6	190	6	US-10-953-349-34143	Sequence 34143, A	763	112.5	3.6	426	6	US-10-953-349-5421	Sequence 5421, Ap
691	114	3.6	195	6	US-10-953-349-35816	Sequence 35816, A	764	112.5	3.6	459	6	US-10-449-902-53360	Sequence 53360, A
692	114	3.6	251	7	US-11-056-355B-4501	Sequence 4501, Ap	765	112.5	3.6	531	6	US-10-953-349-5420	Sequence 5420, Ap
693	114	3.6	275	6	US-10-953-349-1558	Sequence 1558, Ap	766	112.5	3.6	562	7	US-11-056-355B-7605	Sequence 7605, Ap
694	114	3.6	275	7	US-11-056-355B-21327	Sequence 21327, A	767	112.5	3.6	564	7	US-11-056-355B-7604	Sequence 7604, Ap
695	114	3.6	275	7	US-11-056-355B-25213	Sequence 25213, A	768	112.5	3.6	574	6	US-10-953-349-12942	Sequence 12942, A
696	114	3.6	275	7	US-11-056-355B-38933	Sequence 38933, A	769	112.5	3.6	574	6	US-10-449-902-40978	Sequence 40978, A
697	114	3.6	275	7	US-11-056-355B-101263	Sequence 101263, A	770	112.5	3.6	630	6	US-10-449-902-40978	Sequence 40978, A
698	114	3.6	275	7	US-11-056-355B-101262	Sequence 101262, A	771	112.5	3.6	636	6	US-10-539-228-428	Sequence 428, App
699	114	3.6	322	7	US-11-056-355B-72399	Sequence 72399, A	772	112.5	3.6	637	6	US-10-953-349-12941	Sequence 12941, A
700	114	3.6	372	6	US-10-953-349-1557	Sequence 1557, Ap	773	112.5	3.6	638	6	US-10-953-349-12940	Sequence 12940, A
701	114	3.6	372	7	US-11-056-355B-21326	Sequence 21326, A	774	112.5	3.6	720	6	US-10-539-228-432	Sequence 432, App
702	114	3.6	372	7	US-11-056-355B-25212	Sequence 25212, A	775	112.5	3.6	754	6	US-10-953-349-9200	Sequence 9200, Ap
703	114	3.6	372	7	US-11-056-355B-38932	Sequence 38932, A	776	112.5	3.6	772	7	US-11-056-355B-75114	Sequence 75114, A
704	114	3.6	372	7	US-11-056-355B-101262	Sequence 101262, A	777	112.5	3.6	772	7	US-11-056-355B-96477	Sequence 96477, A
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706	114	3.6	381	6	US-10-953-349-1556	Sequence 1556, Ap	779	112	3.6	240	6	US-10-953-349-18175	Sequence 18175, A
707	114	3.6	381	7	US-11-056-355B-21325	Sequence 21325, A	780	112	3.6	240	6	US-11-056-355B-59359	Sequence 59359, A
708	114	3.6	381	7	US-11-056-355B-25211	Sequence 25211, A	781	112	3.6	246	6	US-10-953-349-18174	Sequence 18174, A
709	114	3.6	381	7	US-11-056-355B-38931	Sequence 38931, A	782	112	3.6	246	6	US-11-056-355B-99358	Sequence 99358, A
710	114	3.6	381	7	US-11-056-355B-101261	Sequence 101261, A	783	112	3.6	275	7	US-11-056-355B-22076	Sequence 22076, A
711	114	3.6	381	7	US-11-056-355B-112500	Sequence 112500, A	784	112	3.6	293	7	US-11-056-355B-22075	Sequence 22075, A
712	114	3.6	413	6	US-10-511-937-2428	Sequence 2428, Ap	785	112	3.6	318	6	US-10-953-349-27976	Sequence 27976, A
713	114	3.6	620	7	US-11-293-697-3458	Sequence 3458, Ap	786	112	3.6	334	6	US-10-953-349-27975	Sequence 27975, A
714	114	3.6	620	7	US-10-449-902-53399	Sequence 53399, A	787	112	3.6	334	6	US-10-953-349-27975	Sequence 27975, A
715	114	3.6	691	6	US-10-449-902-45030	Sequence 45030, A	788	112	3.6	334	6	US-11-056-355B-69073	Sequence 69073, A
716	113.5	3.6	159	6	US-10-953-349-34145	Sequence 34145, A	789	112	3.6	355	6	US-10-953-349-27974	Sequence 27974, A
717	113.5	3.6	179	6	US-10-953-349-27151	Sequence 27151, A	790	112	3.6	355	6	US-11-056-355B-69072	Sequence 69072, A
718	113.5	3.6	179	6	US-11-056-355B-63083	Sequence 63083, A	791	112	3.6	382	6	US-10-953-349-16918	Sequence 16918, A
719	113.5	3.6	218	6	US-10-953-349-27150	Sequence 27150, A	792	112	3.6	542	6	US-10-449-902-42550	Sequence 42550, A
720	113.5	3.6	218	7	US-11-056-355B-63082	Sequence 63082, A	793	112	3.6	641	6	US-10-449-902-47052	Sequence 47052, A
721	113.5	3.6	289	7	US-11-056-355B-63092	Sequence 63092, A	794	112	3.6	731	7	US-11-056-355B-80297	Sequence 80297, A
722	113.5	3.6	300	7	US-11-056-355B-62375	Sequence 62375, A	795	112	3.6	785	6	US-10-537-258A-6029	Sequence 63, Appl
723	113.5	3.6	309	7	US-11-056-355B-62374	Sequence 62374, A	796	112	3.6	864	7	US-11-178-724-27	Sequence 27, Appl
724	113.5	3.6	335	6	US-10-449-902-41536	Sequence 41536, A	797	112	3.6	1014	7	US-11-056-355B-72514	Sequence 72514, A
725	113.5	3.6	534	7	US-11-056-355B-88146	Sequence 88146, A	798	112	3.6	1015	7	US-11-056-355B-72513	Sequence 72513, A
726	113.5	3.6	601	7	US-11-293-697-4589	Sequence 4589, Ap	799	112	3.6	1019	7	US-11-056-355B-72512	Sequence 72512, A
727	113.5	3.6	635	7	US-11-056-355B-17644	Sequence 17644, A	800	112	3.6	1066	6	US-10-449-902-43289	Sequence 43289, A
728	113.5	3.6	638	7	US-11-174-307B-3660	Sequence 3660, Ap	801	111.5	3.6	315	6	US-10-953-349-28294	Sequence 28294, A
729	113.5	3.6	907	7	US-11-056-355B-107030	Sequence 107030, A	802	111.5	3.6	315	7	US-11-056-355B-62479	Sequence 62479, A
730	113.5	3.6	1007	7	US-11-056-355B-118269	Sequence 118269, A	803	111.5	3.6	452	6	US-10-953-349-8194	Sequence 8194, Ap
731	113.5	3.6	1008	7	US-11-288-992-11	Sequence 11, Appl	804	111.5	3.6	460	6	US-10-953-349-8193	Sequence 8193, Ap
732	113.5	3.6	1021	6	US-10-449-902-48223	Sequence 48223, A	805	111.5	3.6	498	7	US-11-056-355B-19162	Sequence 19162, A
733	113.5	3.6	1034	7	US-11-288-992-47	Sequence 47, Appl	806	111.5	3.6	593	6	US-11-056-355B-17091	Sequence 17091, A
734	113.5	3.6	1113	7	US-11-056-355B-77057	Sequence 77057, A	807	111.5	3.6	647	7	US-11-330-403-18712	Sequence 18712, A
735	113	3.6	193	6	US-10-953-349-36904	Sequence 36904, A	808	111.5	3.6	656	6	US-10-517-420-50	Sequence 50, Appl
736	113	3.6	262	6	US-10-953-349-16177	Sequence 16177, A	809	111.5	3.6	662	6	US-10-449-902-40037	Sequence 40037, A
737	113	3.6	274	6	US-10-953-349-16176	Sequence 16176, A	810	111.5	3.6	672	6	US-10-449-902-55623	Sequence 55623, A
738	113	3.6	275	6	US-10-953-349-1384	Sequence 1384, Ap	811	111.5	3.6	678	6	US-10-517-420-52	Sequence 52, Appl
739	113	3.6	276	7	US-11-056-355B-3034	Sequence 3034, Ap	812	111.5	3.6	832	7	US-11-056-355B-107032	Sequence 107032, A
740	113	3.6	359	7	US-11-154-977-29	Sequence 29, Appl	813	111.5	3.6	832	7	US-11-056-355B-118271	Sequence 118271, A
741	113	3.6	371	6	US-10-953-349-1353	Sequence 1353, Ap	814	111.5	3.6	858	7	US-11-056-355B-107031	Sequence 107031, A
742	113	3.6	382	7	US-11-056-355B-34852	Sequence 34852, A	815	111.5	3.6	858	7	US-11-056-355B-118270	Sequence 118270, A
743	113	3.6	391	7	US-11-056-355B-34851	Sequence 34851, A	816	111.5	3.6	958	6	US-10-449-902-53356	Sequence 53356, A
744	113	3.6	394	6	US-10-953-349-1352	Sequence 1352, Ap	817	111.5	3.6	1030	7	US-11-056-355B-118275	Sequence 118275, A
745	113	3.6	647	6	US-10-449-902-56469	Sequence 56469, A	818	111.5	3.6	1030	7	US-11-056-355B-118514	Sequence 118514, A
746	113	3.6	864	6	US-10-449-902-41028	Sequence 41028, A	819	111.5	3.6	1073	6	US-10-449-902-41088	Sequence 41088, A
747	113	3.6	899	7	US-11-056-355B-95940	Sequence 95940, A	820	111.5	3.6	1073	7	US-11-056-355B-107274	Sequence 107274, A
748	113	3.6	928	7	US-11-056-355B-95939	Sequence 95939, A	821	111.5	3.6	1073	7	US-11-056-355B-118513	Sequence 118513, A
749	113	3.6	999	7	US-11-056-355B-90832	Sequence 90832, A	822	111	3.5	214	6	US-10-449-902-31897	Sequence 31897, A
750	113	3.6	999	7	US-11-056-355B-94588	Sequence 94588, A	823	111	3.5	274	7	US-11-056-355B-5773	Sequence 5773, Ap
751	113	3.6	1002	7	US-11-056-355B-50734	Sequence 50734, A	824	111	3.5	478	7	US-11-056-355B-84488	Sequence 84488, A
752	113	3.6	1018	7	US-11-056-355B-90831	Sequence 90831, A	825	111	3.5	482	7	US-11-056-355B-84487	Sequence 84487, A
753	113	3.6	1018	7	US-11-056-355B-94587	Sequence 94587, A	826	111	3.5	495	7	US-11-293-697-4277	Sequence 4277, Ap
754	113	3.6	1025	7	US-11-056-355B-90830	Sequence 90830, A	827	111	3.5	617	7	US-11-056-355B-70041	Sequence 70041, A
755	113	3.6	1025	7	US-11-056-355B-94586	Sequence 94586, A	828	111	3.5	706	7	US-11-056-355B-48697	Sequence 48697, A



829	111	3.5	706	7	US-11-056-355B-50499	Sequence 50499, A	902	109.5	3.5	517	7	US-11-174-307B-4664	Sequence 4664, Ap
830	111	3.5	712	7	US-11-056-355B-48696	Sequence 48696, A	903	109.5	3.5	645	6	US-10-449-902-37568	Sequence 37568, A
831	111	3.5	712	7	US-11-056-355B-50498	Sequence 50498, A	904	109.5	3.5	690	7	US-11-330-403-4570	Sequence 4570, Ap
832	111	3.5	771	7	US-11-056-355B-72906	Sequence 72906, A	905	109.5	3.5	839	7	US-11-326-389-14	Sequence 14, Appl
833	110.5	3.5	269	7	US-11-056-355B-2619	Sequence 2619, Ap	906	109.5	3.5	1418	7	US-11-217-997-38	Sequence 38, Appl
834	110.5	3.5	312	6	US-10-953-349-31493	Sequence 31493, A	907	109.5	3.5	1866	6	US-10-511-937-2368	Sequence 2966, Ap
835	110.5	3.5	312	6	US-11-056-355B-68325	Sequence 68325, A	908	109	3.5	182	7	US-11-056-355B-8304	Sequence 8304, Ap
836	110.5	3.5	319	7	US-11-056-355B-20183	Sequence 20183, A	909	109	3.5	259	7	US-11-293-697-4741	Sequence 4741, Ap
837	110.5	3.5	346	7	US-11-036-257-33	Sequence 33, Appl	910	109	3.5	329	6	US-10-953-349-23958	Sequence 23958, A
838	110.5	3.5	376	6	US-10-953-349-34877	Sequence 34877, A	911	109	3.5	329	6	US-11-056-355B-58321	Sequence 58321, A
839	110.5	3.5	376	7	US-11-056-355B-3057	Sequence 3057, Ap	912	109	3.5	416	6	US-10-505-928-276	Sequence 276, App
840	110.5	3.5	376	7	US-11-056-355B-20271	Sequence 20271, A	913	109	3.5	443	7	US-10-505-928-276	Sequence 276, App
841	110.5	3.5	379	6	US-10-953-349-34876	Sequence 34876, A	914	109	3.5	475	7	US-11-056-355B-97045	Sequence 97045, A
842	110.5	3.5	379	7	US-11-056-355B-3056	Sequence 3056, Ap	915	109	3.5	495	6	US-10-953-349-7418	Sequence 7418, Ap
843	110.5	3.5	379	7	US-11-056-355B-20270	Sequence 20270, A	916	109	3.5	598	6	US-10-953-349-7417	Sequence 7417, Ap
844	110.5	3.5	394	6	US-10-449-902-33848	Sequence 33848, A	917	109	3.5	598	6	US-10-953-349-9928	Sequence 9928, Ap
845	110.5	3.5	394	6	US-10-449-902-36841	Sequence 36841, A	918	109	3.5	866	6	US-10-953-349-9927	Sequence 9927, Ap
846	110.5	3.5	394	6	US-10-449-902-40453	Sequence 40453, A	919	109	3.5	866	6	US-10-953-349-9927	Sequence 9927, Ap
847	110.5	3.5	394	6	US-10-449-902-46114	Sequence 46114, A	920	109	3.5	951	6	US-10-953-349-9926	Sequence 9926, Ap
848	110.5	3.5	411	7	US-11-036-257-89	Sequence 89, Appl	921	109	3.5	1278	6	US-10-486-020-8	Sequence 8, Appl
849	110.5	3.5	418	6	US-10-953-349-34875	Sequence 34875, A	922	109	3.5	1358	6	US-10-528-542-23	Sequence 23, Appl
850	110.5	3.5	418	7	US-11-056-355B-3055	Sequence 3055, Ap	923	108.5	3.5	160	7	US-11-056-355B-8305	Sequence 8305, Ap
851	110.5	3.5	418	7	US-11-056-355B-20269	Sequence 20269, A	924	108.5	3.5	315	6	US-10-449-902-35365	Sequence 35365, A
852	110.5	3.5	577	7	US-11-293-697-3929	Sequence 3929, Ap	925	108.5	3.5	393	6	US-10-449-902-35570	Sequence 35570, A
853	110.5	3.5	606	7	US-11-056-355B-69816	Sequence 69816, A	926	108.5	3.5	402	7	US-11-056-355B-40984	Sequence 40984, A
854	110.5	3.5	622	6	US-10-449-902-55221	Sequence 55221, A	927	108.5	3.5	416	7	US-11-293-697-4319	Sequence 4319, Ap
855	110.5	3.5	630	6	US-10-449-902-42293	Sequence 42293, A	928	108.5	3.5	445	7	US-11-056-355B-19163	Sequence 19163, A
856	110.5	3.5	643	6	US-10-505-928-249	Sequence 249, App	929	108.5	3.5	767	6	US-10-449-902-56749	Sequence 56749, A
857	110.5	3.5	684	7	US-11-056-355B-14442	Sequence 14442, A	930	108.5	3.5	940	6	US-10-449-902-41416	Sequence 41416, A
858	110.5	3.5	714	7	US-11-056-355B-80298	Sequence 80298, A	931	108.5	3.5	1125	7	US-11-252-276-152	Sequence 152, App
859	110.5	3.5	809	7	US-11-056-355B-72899	Sequence 72899, A	932	108.5	3.5	1255	7	US-11-105-233-184	Sequence 184, App
860	110.5	3.5	1006	7	US-11-056-355B-72897	Sequence 72897, A	933	108	3.5	1610	6	US-10-449-902-37046	Sequence 37046, A
861	110.5	3.5	1243	6	US-10-449-902-41332	Sequence 41332, A	934	108	3.4	256	6	US-10-449-902-37138	Sequence 37138, A
862	110.5	3.5	216	6	US-10-449-902-39091	Sequence 39091, A	935	108	3.4	316	6	US-10-449-902-36074	Sequence 36074, A
863	110	3.5	275	7	US-11-056-355B-40593	Sequence 40593, A	936	108	3.4	428	7	US-11-056-355B-3391	Sequence 3391, Ap
864	110	3.5	275	7	US-11-056-355B-104448	Sequence 104448, A	937	108	3.4	476	6	US-10-449-902-47026	Sequence 47026, A
865	110	3.5	275	7	US-11-056-355B-115687	Sequence 115687, A	938	108	3.4	599	6	US-10-547-207-15	Sequence 15, Appl
866	110	3.5	374	7	US-11-056-355B-38684	Sequence 38684, A	939	108	3.4	638	7	US-11-330-403-15603	Sequence 15603, A
867	110	3.5	401	6	US-10-449-902-39779	Sequence 39779, A	940	108	3.4	671	6	US-10-449-902-54834	Sequence 54834, A
868	110	3.5	440	6	US-10-449-902-40711	Sequence 40711, A	941	108	3.4	715	7	US-11-056-355B-79053	Sequence 79053, A
869	110	3.5	459	7	US-11-056-355B-5415	Sequence 5415, Ap	942	108	3.4	776	6	US-10-449-902-41391	Sequence 41391, A
870	110	3.5	467	7	US-11-246-999-34	Sequence 34, Appl	943	108	3.4	995	7	US-11-246-999-48	Sequence 48, Appl
871	110	3.5	550	6	US-10-953-349-22717	Sequence 22717, A	944	108	3.4	1730	7	US-11-270-040-6	Sequence 6, Appl
872	110	3.5	550	7	US-11-297-315-30	Sequence 30, Appl	945	107.5	3.4	239	7	US-11-056-355B-12545	Sequence 12545, A
873	110	3.5	550	7	US-10-449-902-43264	Sequence 43264, A	946	107.5	3.4	306	6	US-10-953-349-33730	Sequence 33730, A
874	110	3.5	578	6	US-10-449-902-46835	Sequence 46835, A	947	107.5	3.4	333	6	US-10-449-902-54335	Sequence 54335, A
875	110	3.5	578	6	US-11-358-419-43	Sequence 419, Appl	948	107.5	3.4	378	6	US-10-449-902-48084	Sequence 48084, A
876	110	3.5	626	7	US-11-378-923-23	Sequence 23, Appl	949	107.5	3.4	394	6	US-10-449-902-52557	Sequence 52557, A
877	110	3.5	626	7	US-11-378-923-24	Sequence 24, Appl	950	107.5	3.4	416	6	US-11-056-355B-16321	Sequence 16321, A
878	110	3.5	708	7	US-11-056-355B-90579	Sequence 90579, A	951	107.5	3.4	447	6	US-10-449-902-37103	Sequence 37103, A
879	110	3.5	708	7	US-11-056-355B-94335	Sequence 94335, A	952	107.5	3.4	447	6	US-10-449-902-54102	Sequence 54102, A
880	110	3.5	811	6	US-10-953-349-4751	Sequence 4751, Ap	953	107.5	3.4	447	6	US-10-449-902-56107	Sequence 56107, A
881	110	3.5	811	6	US-10-953-349-4751	Sequence 4751, Ap	954	107.5	3.4	492	6	US-10-449-902-42619	Sequence 42619, A
882	110	3.5	922	6	US-10-953-349-4750	Sequence 4750, Ap	955	107.5	3.4	656	7	US-11-293-697-2611	Sequence 2611, Ap
883	110	3.5	1030	6	US-10-449-902-41538	Sequence 41538, A	956	107.5	3.4	713	6	US-10-449-902-41723	Sequence 41723, A
884	110	3.5	1123	6	US-10-953-349-4749	Sequence 4749, Ap	957	107.5	3.4	723	7	US-11-178-724-18	Sequence 18, Appl
885	110	3.5	1551	6	US-10-449-902-41326	Sequence 41326, A	958	107.5	3.4	723	7	US-11-071-796A-17	Sequence 17, Appl
886	109.5	3.5	148	6	US-10-449-902-48536	Sequence 48536, A	959	107.5	3.4	765	7	US-11-292-634-2	Sequence 2, Appl
887	109.5	3.5	191	7	US-11-056-355B-84744	Sequence 84744, A	960	107.5	3.4	900	7	US-11-056-355B-90828	Sequence 90828, A
888	109.5	3.5	288	6	US-10-953-349-22296	Sequence 22296, A	961	107.5	3.4	900	7	US-11-056-355B-94584	Sequence 94584, A
889	109.5	3.5	301	6	US-11-056-355B-62481	Sequence 62481, A	962	107.5	3.4	949	7	US-11-056-355B-49856	Sequence 49856, A
890	109.5	3.5	315	6	US-10-449-902-49685	Sequence 49685, A	963	107.5	3.4	949	7	US-11-056-355B-83268	Sequence 83268, A
891	109.5	3.5	352	6	US-10-540-845-6	Sequence 6, Appl	964	107.5	3.4	997	7	US-11-056-355B-90827	Sequence 90827, A
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893	109.5	3.5	357	6	US-10-540-845-9	Sequence 9, Appl	966	107.5	3.4	1006	7	US-11-056-355B-83267	Sequence 83267, A
894	109.5	3.5	357	6	US-10-540-845-4	Sequence 4, Appl	967	107.5	3.4	1009	7	US-11-056-355B-90826	Sequence 90826, A
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896	109.5	3.5	386	6	US-11-154-977-19	Sequence 19, Appl	969	107.5	3.4	1021	7	US-11-056-355B-49855	Sequence 49855, A
897	109.5	3.5	386	6	US-10-540-845-10	Sequence 10, Appl	970	107	3.4	255	6	US-10-449-902-56595	Sequence 56595, A
898	109.5	3.5	390	6	US-10-953-349-17661	Sequence 17661, A	971	107	3.4	275	7	US-11-056-355B-75718	Sequence 75718, A
899	109.5	3.5	426	7	US-11-174-307B-4268	Sequence 4268, Ap	972	107	3.4	450	6	US-10-449-902-37895	Sequence 37895, A
900	109.5	3.5	426	7	US-11-056-355B-42592	Sequence 42592, A	973	107	3.4	535	6	US-10-449-902-45304	Sequence 45304, A
901	109.5	3.5	428	7	US-11-056-355B-42592	Sequence 42592, A	974	107	3.4	609	7	US-11-056-355B-17645	Sequence 17645, A



975	107	3.4	1034	6	US-10-449-902-41078	Sequence 41078, A	1048	104.5	3.3	198	6	US-10-953-349-37387	Sequence 37387, A
976	107	3.4	1307	6	US-10-449-902-43546	Sequence 43546, A	1049	104.5	3.3	219	7	US-11-056-355B-91556	Sequence 91556, A
977	106.5	3.4	170	7	US-11-056-355B-9953	Sequence 9953, Ap	1050	104.5	3.3	219	7	US-11-056-355B-95412	Sequence 95412, A
978	106.5	3.4	193	7	US-11-056-355B-50252	Sequence 50252, A	1051	104.5	3.3	221	6	US-10-953-349-36059	Sequence 36059, A
979	106.5	3.4	196	6	US-10-449-902-42354	Sequence 42354, A	1052	104.5	3.3	221	7	US-11-056-355B-8636	Sequence 8636, Ap
980	106.5	3.4	224	7	US-11-056-355B-1830	Sequence 1830, Ap	1053	104.5	3.3	267	6	US-10-953-349-37386	Sequence 37386, A
981	106.5	3.4	229	6	US-10-449-902-39832	Sequence 39832, A	1054	104.5	3.3	276	7	US-11-056-355B-6311	Sequence 6311, Ap
982	106.5	3.4	294	7	US-11-056-355B-1829	Sequence 1829, Ap	1055	104.5	3.3	367	7	US-11-056-355B-14743	Sequence 14743, A
983	106.5	3.4	328	7	US-11-056-355B-1828	Sequence 1828, Ap	1056	104.5	3.3	685	7	US-11-056-355B-47029	Sequence 47029, A
984	106.5	3.4	376	7	US-11-056-355B-16351	Sequence 16351, A	1057	104.5	3.3	705	6	US-10-449-902-47238	Sequence 47238, A
985	106.5	3.4	642	7	US-11-175-714-10	Sequence 10, Appl	1058	104.5	3.3	901	7	US-11-293-697-2845	Sequence 2845, Ap
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987	106.5	3.4	912	6	US-10-449-902-43619	Sequence 43619, A	1060	104.5	3.3	1479	7	US-11-056-355B-82452	Sequence 82452, A
988	106	3.4	128	7	US-11-056-355B-10528	Sequence 10528, A	1061	104.5	3.3	1544	7	US-11-056-355B-82451	Sequence 82451, A
989	106	3.4	142	6	US-10-449-902-47994	Sequence 47994, A	1062	104.5	3.3	1601	7	US-11-056-355B-82451	Sequence 40, Appl
990	106	3.4	188	6	US-10-953-349-32350	Sequence 2350, A	1063	104	3.3	157	6	US-11-358-419-40	Sequence 37993, A
991	106	3.4	312	6	US-10-449-902-34826	Sequence 34826, A	1064	104	3.3	306	7	US-11-241-106-7	Sequence 7, Appl
992	106	3.4	418	6	US-10-449-902-39915	Sequence 39915, A	1065	104	3.3	320	7	US-11-056-355B-8066	Sequence 8066, Ap
993	106	3.4	626	7	US-11-293-697-3922	Sequence 3922, Ap	1066	104	3.3	320	7	US-11-056-355B-15719	Sequence 15719, A
994	106	3.4	653	7	US-10-449-902-52932	Sequence 52932, A	1067	104	3.3	365	7	US-11-251-643-2	Sequence 2, Appl
995	106	3.4	814	7	US-11-242-617-2	Sequence 2, Appl	1068	104	3.3	384	6	US-10-505-928-395	Sequence 395, App
996	106	3.4	830	7	US-11-056-355B-95941	Sequence 95941, A	1069	104	3.3	400	7	US-11-174-307B-3754	Sequence 3754, Ap
997	106	3.4	830	7	US-11-175-714-11	Sequence 11, Appl	1070	104	3.3	437	7	US-10-953-349-27432	Sequence 27432, A
998	106	3.4	862	6	US-10-953-349-13625	Sequence 13625, A	1071	104	3.3	437	7	US-11-293-697-3507	Sequence 3507, Ap
999	106	3.4	928	7	US-11-056-355B-107694	Sequence 107694, A	1072	104	3.3	491	7	US-11-293-697-4290	Sequence 4290, Ap
1000	106	3.4	928	7	US-11-056-355B-118933	Sequence 118933, A	1073	104	3.3	496	7	US-11-293-697-2541	Sequence 2541, Ap
1001	106	3.4	945	7	US-11-056-355B-107693	Sequence 107693, A	1074	104	3.3	638	7	US-11-056-355B-96479	Sequence 96479, A
1002	106	3.4	945	7	US-11-056-355B-118932	Sequence 118932, A	1075	104	3.3	671	7	US-11-056-355B-96478	Sequence 96478, A
1003	106	3.4	971	7	US-11-056-355B-107692	Sequence 107692, A	1076	104	3.3	678	7	US-10-449-902-32624	Sequence 32624, A
1004	106	3.4	971	7	US-11-056-355B-118931	Sequence 118931, A	1077	104	3.3	771	6	US-10-449-902-41433	Sequence 41433, A
1005	106	3.4	1356	6	US-10-480-962-16	Sequence 16, Appl	1078	104	3.3	1159	6	US-10-449-902-41184	Sequence 41184, A
1006	105.5	3.4	127	6	US-10-449-902-32490	Sequence 32490, A	1079	104	3.3	1169	6	US-10-449-902-41184	Sequence 36060, A
1007	105.5	3.4	202	6	US-10-953-349-28727	Sequence 28727, A	1080	103.5	3.3	216	6	US-10-953-349-36060	Sequence 6637, Ap
1008	105.5	3.4	240	7	US-11-056-355B-39682	Sequence 39682, A	1081	103.5	3.3	217	7	US-11-056-355B-8637	Sequence 8637, Ap
1009	105.5	3.4	246	6	US-10-449-902-29576	Sequence 29576, A	1082	103.5	3.3	246	7	US-11-056-355B-64487	Sequence 64487, A
1010	105.5	3.4	246	6	US-10-449-902-54201	Sequence 54201, A	1083	103.5	3.3	294	6	US-10-953-349-25258	Sequence 25258, A
1011	105.5	3.4	246	6	US-10-449-902-56517	Sequence 56517, A	1084	103.5	3.3	304	6	US-10-449-902-56429	Sequence 56429, A
1012	105.5	3.4	286	7	US-11-056-355B-82540	Sequence 82540, A	1085	103.5	3.3	314	6	US-10-953-349-25257	Sequence 25257, A
1013	105.5	3.4	291	7	US-11-056-355B-3800	Sequence 3800, Ap	1086	103.5	3.3	317	6	US-10-953-349-1704	Sequence 1704, Ap
1014	105.5	3.4	323	7	US-11-293-697-4625	Sequence 4625, Ap	1087	103.5	3.3	317	7	US-11-056-355B-29982	Sequence 29982, A
1015	105.5	3.4	325	7	US-11-056-355B-7510	Sequence 7510, Ap	1088	103.5	3.3	317	7	US-11-056-355B-33572	Sequence 33572, A
1016	105.5	3.4	336	7	US-11-056-355B-8065	Sequence 8065, Ap	1089	103.5	3.3	353	6	US-10-953-349-8195	Sequence 8195, Ap
1017	105.5	3.4	336	7	US-11-056-355B-15718	Sequence 15718, A	1090	103.5	3.3	363	7	US-11-056-355B-62800	Sequence 62800, A
1018	105.5	3.4	341	6	US-11-056-355B-7509	Sequence 7509, Ap	1091	103.5	3.3	367	6	US-10-953-349-1703	Sequence 1703, Ap
1019	105.5	3.4	384	7	US-10-449-902-41009	Sequence 41009, A	1092	103.5	3.3	367	7	US-11-056-355B-29981	Sequence 29981, A
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1021	105.5	3.4	403	7	US-11-056-355B-39681	Sequence 39681, A	1094	103.5	3.3	367	7	US-11-330-403-1547	Sequence 1547, Ap
1022	105.5	3.4	404	7	US-11-056-355B-39680	Sequence 39680, A	1095	103.5	3.3	367	7	US-11-330-403-18119	Sequence 18119, A
1023	105.5	3.4	457	7	US-11-375-414-110	Sequence 110, App	1096	103.5	3.3	400	6	US-10-953-349-37484	Sequence 37484, A
1024	105.5	3.4	824	7	US-11-293-697-4085	Sequence 4085, Ap	1097	103.5	3.3	400	7	US-11-056-355B-82727	Sequence 82727, A
1025	105.5	3.4	824	7	US-11-293-697-3650	Sequence 3650, Ap	1098	103.5	3.3	402	7	US-11-274-634-18	Sequence 18, Appl
1026	105.5	3.4	2220	7	US-11-251-643-14	Sequence 14, Appl	1099	103.5	3.3	407	7	US-11-056-355B-62799	Sequence 62799, A
1027	105	3.3	173	7	US-11-217-997-36	Sequence 36, Appl	1100	103.5	3.3	412	7	US-11-056-355B-8069	Sequence 8069, Ap
1028	105	3.3	190	6	US-10-953-349-15678	Sequence 15678, A	1101	103.5	3.3	417	6	US-10-953-349-37483	Sequence 37483, A
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1032	105	3.3	276	7	US-11-056-355B-39971	Sequence 39971, A	1105	103.5	3.3	670	7	US-11-056-355B-118888	Sequence 118888, A
1033	105	3.3	276	7	US-11-056-355B-83851	Sequence 83851, A	1106	103.5	3.3	675	6	US-10-519-135-45	Sequence 45, Appl
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1038	105	3.3	383	7	US-11-056-355B-39969	Sequence 39969, A	1111	103.5	3.3	947	7	US-11-056-355B-82395	Sequence 82395, A
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1046	104.5	3.3	157	7	US-11-175-714-6	Sequence 6, Appl	1119	103.5	3.3	1556	7	US-11-056-355B-86187	Sequence 86187, A
1047	104.5	3.3	181	6	US-10-449-902-44231	Sequence 44231, A	1120	103.5	3.3	1556	7	US-11-056-355B-86187	Sequence 86187, A



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1126	103	3.3	263	7	US-11-056-355B-6312	Sequence 6312, Ap	1199	102	3.3	269	7	US-11-056-355B-97886	Sequence 97886, A
1127	103	3.3	335	6	US-10-449-902-29697	Sequence 29697, A	1200	102	3.3	269	7	US-11-056-355B-109125	Sequence 109125, A
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1131	103	3.3	410	7	US-11-056-355B-3392	Sequence 3392, Ap	1204	102	3.3	477	7	US-11-056-355B-84651	Sequence 84651, A
1132	103	3.3	496	7	US-11-056-355B-46181	Sequence 46181, A	1205	102	3.3	497	7	US-11-056-355B-84650	Sequence 84650, A
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1134	103	3.3	554	7	US-11-242-111-20	Sequence 20, Appli	1207	102	3.3	508	7	US-11-293-697-3028	Sequence 3028, Ap
1135	103	3.3	605	6	US-10-953-349-32398	Sequence 32398, A	1208	102	3.3	534	7	US-11-056-355B-84649	Sequence 84649, A
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1137	103	3.3	610	7	US-11-056-355B-34388	Sequence 34388, A	1210	102	3.3	705	7	US-11-056-355B-50736	Sequence 50736, A
1138	103	3.3	610	7	US-11-056-355B-45696	Sequence 45696, A	1211	102	3.3	721	7	US-11-056-355B-50735	Sequence 50735, A
1139	103	3.3	611	7	US-11-056-355B-46180	Sequence 46180, A	1212	102	3.3	720	7	US-11-175-714-4	Sequence 4, Appli
1140	103	3.3	611	7	US-11-056-355B-48883	Sequence 48883, A	1213	102	3.3	729	7	US-11-175-714-8	Sequence 8, Appli
1141	103	3.3	615	7	US-11-056-355B-30797	Sequence 30797, A	1214	102	3.3	798	7	US-11-292-634-6	Sequence 6, Appli
1142	103	3.3	615	7	US-11-056-355B-34387	Sequence 34387, A	1215	102	3.3	1007	6	US-10-519-342-4	Sequence 4, Appli
1143	103	3.3	615	7	US-11-056-355B-45695	Sequence 45695, A	1216	102	3.3	1024	6	US-10-449-902-46823	Sequence 46823, A
1144	103	3.3	677	7	US-11-056-355B-46179	Sequence 46179, A	1217	102	3.3	1247	7	US-11-330-403-18943	Sequence 18943, A
1145	103	3.3	677	7	US-11-056-355B-48882	Sequence 48882, A	1218	102	3.3	3696	7	US-11-330-363-4	Sequence 4, Appli
1146	103	3.3	695	6	US-10-539-228-376	Sequence 376, App	1219	101.5	3.2	155	6	US-10-953-349-15526	Sequence 15526, A
1147	103	3.3	881	6	US-10-539-228-374	Sequence 374, App	1220	101.5	3.2	164	6	US-10-953-349-22367	Sequence 22367, A
1148	103	3.3	928	6	US-10-449-902-41341	Sequence 41341, A	1221	101.5	3.2	173	6	US-10-953-349-15525	Sequence 15525, A
1149	103	3.3	935	6	US-10-449-902-44414	Sequence 44414, A	1222	101.5	3.2	180	6	US-10-953-349-22366	Sequence 22366, A
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1153	103	3.3	1201	7	US-11-056-355B-46396	Sequence 46396, A	1226	101.5	3.2	340	7	US-11-259-133-54	Sequence 54, Appli
1154	103	3.3	1207	7	US-11-105-233-186	Sequence 186, App	1227	101.5	3.2	433	6	US-10-449-902-50765	Sequence 50765, A
1155	102.5	3.3	198	6	US-10-953-349-18154	Sequence 18154, A	1228	101.5	3.2	577	6	US-10-449-902-53690	Sequence 52690, A
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1157	102.5	3.3	222	7	US-11-056-355B-65337	Sequence 65337, A	1230	101.5	3.2	692	7	US-11-330-403-9024	Sequence 9024, Ap
1158	102.5	3.3	298	6	US-10-953-349-2724	Sequence 2724, Ap	1231	101.5	3.2	719	6	US-10-449-902-43712	Sequence 43712, A
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1162	102.5	3.3	330	6	US-10-953-349-2723	Sequence 2723, Ap	1235	101.5	3.2	966	6	US-10-449-902-41240	Sequence 41240, A
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1164	102.5	3.3	330	7	US-11-056-355B-72579	Sequence 72579, A	1237	101	3.2	219	7	US-11-056-355B-1126	Sequence 1126, Ap
1170	102.5	3.3	409	7	US-11-056-355B-68164	Sequence 68164, A	1238	101	3.2	244	6	US-10-953-349-2725	Sequence 2725, Ap
1166	102.5	3.3	461	7	US-11-056-355B-68162	Sequence 68162, A	1239	101	3.2	244	7	US-11-056-355B-42503	Sequence 42503, A
1167	102.5	3.3	575	7	US-11-287-157A-254	Sequence 254, App	1240	101	3.2	244	7	US-11-056-355B-72581	Sequence 72581, A
1168	102.5	3.3	637	7	US-11-289-102-335	Sequence 335, App	1241	101	3.2	279	6	US-10-449-902-33085	Sequence 33085, A
1169	102.5	3.3	656	7	US-11-056-355B-89084	Sequence 89084, A	1242	101	3.2	291	7	US-11-056-355B-16400	Sequence 16400, A
1171	102.5	3.3	656	7	US-11-056-355B-92840	Sequence 92840, A	1243	101	3.2	343	7	US-11-056-355B-58826	Sequence 58826, A
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1172	102.5	3.3	751	7	US-11-056-355B-88640	Sequence 88640, A	1245	101	3.2	413	7	US-11-056-355B-58825	Sequence 58825, A
1173	102.5	3.3	751	7	US-11-056-355B-88644	Sequence 88644, A	1246	101	3.2	442	7	US-11-056-355B-58824	Sequence 58824, A
1174	102.5	3.3	751	7	US-11-056-355B-92396	Sequence 92396, A	1247	101	3.2	443	6	US-10-511-937-2464	Sequence 2464, Ap
1175	102.5	3.3	751	7	US-11-056-355B-92400	Sequence 92400, A	1248	101	3.2	443	7	US-11-289-102-300	Sequence 300, App
1176	102.5	3.3	774	7	US-11-056-355B-90281	Sequence 90281, A	1249	101	3.2	443	7	US-11-289-102-354	Sequence 354, App
1177	102.5	3.3	774	7	US-11-056-355B-90280	Sequence 90280, A	1250	101	3.2	443	7	US-11-289-102-379	Sequence 379, App
1178	102.5	3.3	811	7	US-11-056-355B-90280	Sequence 90280, A	1251	101	3.2	448	6	US-10-519-135-20	Sequence 20, Appli
1179	102.5	3.3	811	7	US-11-056-355B-94036	Sequence 94036, A	1252	101	3.2	461	7	US-11-293-697-3238	Sequence 3238, Ap
1180	102.5	3.3	907	7	US-11-056-355B-90279	Sequence 90279, A	1253	101	3.2	712	7	US-11-105-233-182	Sequence 162, App
1181	102.5	3.3	907	7	US-11-056-355B-94035	Sequence 94035, A	1254	101	3.2	804	6	US-10-449-902-55004	Sequence 55004, A
1182	102.5	3.3	911	7	US-11-056-355B-106453	Sequence 106453, A	1255	101	3.2	929	6	US-10-449-902-56392	Sequence 56392, A
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1184	102.5	3.3	939	6	US-10-449-902-44431	Sequence 44431, A	1257	101	3.2	1274	7	US-11-056-355B-71360	Sequence 71360, A
1185	102.5	3.3	942	7	US-11-056-355B-106452	Sequence 106452, A	1258	101	3.2	1298	6	US-10-449-902-41177	Sequence 41177, A
1186	102.5	3.3	942	7	US-11-056-355B-117691	Sequence 117691, A	1259	101	3.2	1480	7	US-11-056-355B-71359	Sequence 71359, A
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1188	102.5	3.3	1047	7	US-11-293-697-3852	Sequence 3852, Ap	1261	100.5	3.2	187	6	US-10-449-902-33255	Sequence 39255, A
1189	102.5	3.3	1047	7	US-11-288-992-12	Sequence 12, Appli	1262	100.5	3.2	228	7	US-11-036-257-31	Sequence 31, Appli
1190	102.5	3.3	1822	6	US-10-505-928-700	Sequence 700, App	1263	100.5	3.2	256	6	US-10-953-349-35427	Sequence 35427, A
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1192	102	3.3	210	7	US-11-056-355B-56947	Sequence 56947, A	1265	100.5	3.2	274	7	US-11-056-355B-90495	Sequence 90495, A
1193	102	3.3	218	7	US-11-056-355B-21774	Sequence 21774, A	1266	100.5	3.2	274	7	US-11-056-355B-94251	Sequence 94251, A



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1268	100.5	3.2	335	6	US-10-953-349-22556	Sequence 2556, A	1341	99	3.2	374	6	US-10-449-902-35013	Sequence 35013, A
1269	100.5	3.2	338	6	US-10-449-902-36986	Sequence 36986, A	1342	99	3.2	426	7	US-10-449-902-50174	Sequence 50174, A
1270	100.5	3.2	338	6	US-10-449-902-37100	Sequence 37100, A	1343	99	3.2	397	7	US-11-293-697-2833	Sequence 2833, Ap
1271	100.5	3.2	391	6	US-10-449-902-40132	Sequence 40132, A	1344	99	3.2	536	7	US-11-330-403-7245	Sequence 7245, Ap
1272	100.5	3.2	402	7	US-11-056-355B-13690	Sequence 13690, A	1345	99	3.2	575	6	US-10-953-349-13351	Sequence 13351, A
1273	100.5	3.2	440	6	US-10-449-902-52131	Sequence 52131, A	1346	99	3.2	631	7	US-11-056-355B-25434	Sequence 25434, A
1274	100.5	3.2	441	7	US-11-330-403-7841	Sequence 7841, Ap	1347	99	3.2	632	7	US-11-056-355B-25433	Sequence 25433, A
1275	100.5	3.2	464	6	US-10-953-349-32673	Sequence 32673, A	1348	99	3.2	638	7	US-11-056-355B-25432	Sequence 25432, A
1276	100.5	3.2	464	6	US-11-056-355B-68075	Sequence 68075, A	1349	99	3.2	641	7	US-11-056-355B-97414	Sequence 97414, A
1277	100.5	3.2	610	6	US-10-449-902-55889	Sequence 52889, A	1350	99	3.2	649	7	US-11-056-355B-97414	Sequence 97414, A
1278	100.5	3.2	616	7	US-11-056-355B-58993	Sequence 58993, A	1351	99	3.2	686	7	US-11-330-403-11868	Sequence 11868, A
1279	100.5	3.2	640	6	US-10-449-902-56478	Sequence 56478, A	1352	99	3.2	751	7	US-11-056-355B-91413	Sequence 91413, A
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1281	100.5	3.2	737	7	US-11-296-092-15	Sequence 15, Appl	1355	99	3.2	769	7	US-11-056-355B-91412	Sequence 91412, A
1282	100.5	3.2	737	7	US-11-296-155-15	Sequence 15, Appl	1356	99	3.2	769	7	US-11-056-355B-95168	Sequence 95168, A
1283	100.5	3.2	826	7	US-11-056-355B-106454	Sequence 106454, A	1357	99	3.2	775	7	US-11-293-697-4433	Sequence 4433, Ap
1284	100.5	3.2	826	7	US-11-056-355B-117693	Sequence 117693, A	1358	99	3.2	815	7	US-11-056-355B-91411	Sequence 91411, A
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ALIGNMENTS

RESULT 1

US-11-296-092-69

Sequence 69, Application US/11296092

Publication No. US20060105427A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Botstein, David

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

APPLICANT: Gurney, Austin

APPLICANT: Hillan, Kenneth

APPLICANT: Kijavini, Ivar

APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P2548PIC1

CURRENT APPLICATION NUMBER: US/11/296,092

CURRENT FILING DATE: 2005-12-07

PRIOR APPLICATION NUMBER: US/09/866,028

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PRIOR APPLICATION NUMBER: 60/069,694

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PRIOR FILING DATE: December 17, 1997

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 69

LENGTH: 598

TYPE: PRT

ORGANISM: Homo Sapien

US-11-296-092-69



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Best Local Similarity 100.0%; Pred. No. 1.5e-186;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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; Publication No. US20060127983A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geurtsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/11/296,155
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: US/09/866,028
```

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; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 69
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-11-296-155-69
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Query Match      100.0%; Score 3135; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 1.5e-186;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MCSRVPLLLPULLLALGPGVQCPCGCGCQSQPQVCTARQGTTPRDPVPPDVTGLYVF 60
DB 1 MCSRVPLLLPULLLALGPGVQCPCGCGCQSQPQVCTARQGTTPRDPVPPDVTGLYVF 60

QY 61 ENGITMDASSFAGLPGQLDLSQNIASRLPRLLLDLSHNSLLALEPGILDNTANVE 120
DB 61 ENGITMDASSFAGLPGQLDLSQNIASRLPRLLLDLSHNSLLALEPGILDNTANVE 120

QY 121 ALRAGLGLQQLDEGLFSRLNLDLDVSDNQLERVPPVIRGLRGLTRLAGNTRIAQL 180
DB 121 ALRAGLGLQQLDEGLFSRLNLDLDVSDNQLERVPPVIRGLRGLTRLAGNTRIAQL 180

QY 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLFPRLRLAAARNPFCVPLSWFGPWVRE 240
DB 181 RPEDLAGLAALQELDVSNLSLOALPGDLSGLFPRLRLAAARNPFCVPLSWFGPWVRE 240

QY 241 SHVTLASPEETRCHFPKNAAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300
DB 241 SHVTLASPEETRCHFPKNAAGRLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL 300

QY 301 APTWLSPTAPATAPSPSTAPPVGPVQPCDPCPSTCLNGTCHLGRHHLACLCPG 360
DB 301 APTWLSPTAPATAPSPSTAPPVGPVQPCDPCPSTCLNGTCHLGRHHLACLCPG 360

QY 361 FTGLYCESOMGQGTSPPTVTPRPSRLTLGTEPVSPSLRVLGRLQYLOGSSVQLRSLR 420
DB 361 FTGLYCESOMGQGTSPPTVTPRPSRLTLGTEPVSPSLRVLGRLQYLOGSSVQLRSLR 420

QY 421 LTYRNLSGPDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPPLGPRVPEGEACGEAHT 480
DB 421 LTYRNLSGPDKRLVTLRLPASLAETVTLQLRPNATYSVCVMPPLGPRVPEGEACGEAHT 480

QY 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGV 540
DB 481 PPAVHSHNAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGV 540

QY 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGGLQSLPHAKPYI 598
DB 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGPPGGLQSLPHAKPYI 598
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RESULT 3



US-11-101-316-16  
; Sequence 16, Application US/11101316  
; Publication No. US20060099657A1  
; GENERAL INFORMATION:  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID  
; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA  
; FILE REFERENCE: P3230R1C17C1  
; CURRENT APPLICATION NUMBER: US/11/101,316  
; CURRENT FILING DATE: 2005-04-06  
; PRIOR APPLICATION NUMBER: 10/063526  
; PRIOR FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: 10/006867  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/23328  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 09/380137  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: 60/087759  
; PRIOR FILING DATE: 1998-06-02  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 16  
; LENGTH: 673  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-101-316-16

Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 2.6e-183;  
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 1 MCSRVPLLLPLLLLALGPGVCGCGCCSQPQTVECTARQGTTPRDPVPPDTVGLYVF 60  
DB 1 MCSRVPLLLPLLLLALGPGVCGCGCCSQPQTVECTARQGTTPRDPVPPDTVGLYVF 60  
QY 61 ENGITWLDASSFAGLQGLDLSQNIAS-----LRLPRLLLDLSHNS 105  
DB 61 ENGITWLDAGSFAGLQGLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120  
QY 91 -----LRLPRLLLDLSHNS 180  
DB 121 RGLRRLERYLGKNRIRHIQPGAFDTLDRLLLEKLQDNEALRALPRLPRLLLDLSHNS 180  
QY 106 LLALEPGILDTANVEALRLAGLQGLDGLFSRLRNLDLDVSDNQLERVPVIRGLRG 165  
DB 181 LLALEPGILDTANVEALRLAGLQGLDGLFSRLRNLDLDVSDNQLERVPVIRGLRG 240  
QY 166 LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLRLAAARNPF 225  
DB 241 LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLRLAAARNPF 300  
QY 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 285  
DB 421 HLCTRHLACLCEGTGLYCESQMGQTRPSTPTVTPRPRSLTLGIEPVSPTSIRVGL 480  
QY 406 QRYLGSSVQLRSLRITYNLSPDKRLVTLRLPASIAEYTVTLQRPNATYSYCVNPLGP 465  
DB 481 QRYLGSSVQLRSLRITYNLSPDKRLVTLRLPASIAEYTVTLQRPNATYSYCVNPLGP 540

QY 466 GRVPEGEACGEAHTPPAVHSNHPVTOAREGNPLLIAPALAAVLLAALAAVGAAYCVR 525  
DB 541 GRVPEGEACGEAHTPPAVHSNHPVTOAREGNPLLIAPALAAVLLAALAAVGAAYCVR 600  
QY 526 RGRMAAAAQDKGVGPGAGPLEGKVPLEPGPKATEGGGEALPSGSECEVPLMGFP 585  
DB 601 RGRMAAAAQDKGVGPGAGPLEGKVPLEPGPKATEGGGEALPSGSECEVPLMGFP 660  
QY 586 PGLQSPHLHAKPYI 598  
DB 661 PGLQSPHLHAKPYI 673

RESULT 4  
US-11-376-673-16  
; Sequence 16, Application US/11376673  
; Publication No. US20060160186A1  
; GENERAL INFORMATION:  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPRESSED IN STOMACH TUMOR AND  
; TITLE OF INVENTION: LUNG TUMOR  
; FILE REFERENCE: P3230R1C165C  
; CURRENT APPLICATION NUMBER: US/11/376,673  
; CURRENT FILING DATE: 2006-03-14  
; PRIOR APPLICATION NUMBER: 10/063742  
; PRIOR FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: 10/006867  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/23328  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 60/170262  
; PRIOR FILING DATE: 1999-12-09  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 16  
; LENGTH: 673  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-376-673-16

Query Match 98.4%; Score 3083.5; DB 7; Length 673;  
Best Local Similarity 88.7%; Pred. No. 2.6e-183;  
Matches 597; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 1 MCSRVPLLLPLLLLALGPGVCGCGCCSQPQTVECTARQGTTPRDPVPPDTVGLYVF 60  
DB 1 MCSRVPLLLPLLLLALGPGVCGCGCCSQPQTVECTARQGTTPRDPVPPDTVGLYVF 60  
QY 61 ENGITWLDASSFAGLQGLDLSQNIAS-----LRLPRLLLDLSHNS 90  
DB 61 ENGITWLDAGSFAGLQGLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETF 120  
QY 91 -----LRLPRLLLDLSHNS 105  
DB 121 RGLRRLERYLGKNRIRHIQPGAFDTLDRLLLEKLQDNEALRALPRLPRLLLDLSHNS 180  
QY 106 LLALEPGILDTANVEALRLAGLQGLDGLFSRLRNLDLDVSDNQLERVPVIRGLRG 165  
DB 181 LLALEPGILDTANVEALRLAGLQGLDGLFSRLRNLDLDVSDNQLERVPVIRGLRG 240  
QY 166 LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLRLAAARNPF 225  
DB 241 LTRLRAGNTRIAQLRPEDLAGLAALQELDVSNLSQALPGDLSGLFPRLRLAAARNPF 300  
QY 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 285  
DB 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTATVPT 360  
QY 286 TRPVREPTALSSSLAPTWSLPTAPATEAPSPSTAPPTVGPVQDCCPPSCLNGGTC 345







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Db 249 FOHLPRGLLSLRGNQLTHLAPFAWGLGALRELEGNRLSQLPTALLEPLHSLEALDL 308
QY 175 --TRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLIAAARNPFCVCPIL- 231
Db 309 SGNELSAHPATFGHLGRLESLRNALSALSGDIFAASPALYRLDLGNGWTCDCRLR 368
QY 232 ---SNFGPMVRESHTVLTASPEETRCHFPKPNAGRLLLELDYAD- - - - -FGCPATTTAT 282
Db 369 GLKRWGMDHWSOGRLLTVF- - -VQCRHPPALRGY- - -LDYLDQOOLONGSCADSPSAS 422
QY 283 VPTTRPVVREPTALSSSLAP- - - - -TW- - - - - - - - - - - - - - - - - - 304
Db 423 LTADRERQPLPTAAGEEMTPAGLAABELPPQLQOQGRFLAGVADGGAARELVGNRSAL 482
QY 305 -LSPTAPATEASPSSTAPPTVGPVPODQPPSTCLNGTCHLGRHHLACLCPGFTG 363
Db 483 RLSRRGPGGLQPSPSVAA- - -AAGPAQSLD- - - - - - - - - - - - - - - - - 510
QY 364 LVCESQMGGRTPSPPTVTPRPSRLTLGIEPVS- - - - -PTSRLRVGLQRY- - - - - 408
Db 511 LHKFPQRGPRTRADPALAEPPTTASPGSAPSPAGDPWQRAKTRHGLGTEHQRRAADSGGA 570
QY 409 - - - - -LQGSVQLRSRLTYRN- - - - -LSGPDKRLVTLR- - - - - 437
Db 571 GLPPLVSDPCDFNKFILCNLTVEAGDASVWAVREHRSRPLCGARFRLFLDFRFGQ 630
QY 438 - - - - -LPASIAEYVTVQLRPNATYSVCVMPLGPRVPEGEERACGEAHTPPAVHSNHA 489
Db 631 PKFHRFVYLPSSDSATLRELRGDTPLYVCVEGLGRV- - - - -C- - - - -PVAPRHC 678
QY 490 P-VTQAREGN- - - - -LPILLIAPALAAVLLAALAAVGAAYCYVRRGRAMAAQAQDKGQ 539
Db 679 AGLVTLPEAGSRGGVDYQLLTLLTVALTLVALLAALAAWASRWLRKLRARR- - - - - 730
QY 540 VQPGAGPLELE- - -GVKVPLE- - -PGKATEGGEA-LPSGSEC- - -EVLPMGFP 584
Db 731 --KGAPVHVHMYSTRRLSRMGTVSDPFGFQSHRPTTVCALEADLIEFP 783

RESULT 7
US-11-030-653-26
; Sequence 26, Application US/11030653
; Publication No. US20060147945A1
; GENERAL INFORMATION:
; APPLICANT: Edmonds, Brian
; APPLICANT: Micanovic, Radmila
; APPLICANT: Ou, Weijia
; APPLICANT: Su, Eric
; APPLICANT: Tschang, Sheng-Hung
; APPLICANT: Wang, He
; TITLE OF INVENTION: Novel secreted proteins and their uses
; FILE REFERENCE: X-14001
; CURRENT APPLICATION NUMBER: US/11/030,653
; CURRENT FILING DATE: 2005-01-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-030-653-26

Query Match 10.1%; Score 316.5; DB 7; Length 713;
Best Local Similarity 23.1%; Pred. No. 3e-12;
Matches 166; Conservative 76; Mismatches 251; Indels 225; Gaps 28;

QY 19 PGVQCGSPGSCQCS-OPQTVFCTARQTTVPDRVDPDTVGLYVFENGITWLDASSFAGLPG 77
Db 52 PPATSCPACSCSQASRVICTRRDLAEVPASIPVNTRYLNLQENGIOVIRDTDFKHLR 111
QY 78 LQLLDLSQNIASLR- - - - -LPRLLDLSHNSLLALEPGLDTAN- - - - - 118
Db 112 LEILQSLKNLVRKIEVGAFNGLPSSLNTLELFDNRLTTPVTOAFEYLSKLRELWLNPNPIE 171
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QY 119 -----VEALRIAGLG-----LQQLDEGLFSRLRLNHLHDLDVSNQLERVVPVIRLGR 165
Db 172 SIPSVAFNVRPSLRRLDLGELKRLVISEAAFEGLVNLRYLNLGMCNLKDIENLTALVR- 230
QY 166 LTRFLAGNTRIAQLRPEDLAGLA- - - - -ALQELDVSNLSL 201
Db 231 LEELELSGN-RULDIRPGSFQGLTSRLKWLMLHQAQVATERNAFDLDLSLEELNLSHNL 289
QY 202 QALPGDLSGLFRLRLAAARNPFCVPLSGFPGVWRESHVTTLASPEET- - - - -RCHFP 257
Db 290 MSLPHDLTTPHLRLERVLHNHPWNCNDVLWLSWMLKET- - - - -VPSNTTCCARCHAPA 344
QY 258 KNAGRLLELDYADGCPATTTTATVTPTRPVVREPTALSSSLATWLSLPT-APATEAPS 316
Db 345 GLKGRYIGELDQSHFTCYA- - - - -PVIVEP- - - - -PTDLNVTGMAAELKC 385
QY 317 PPSTAPPTVGPVPOQDCPPSTCLNGGT- - - - -CHLGRHHLACLCPGEGTGLY-CES 368
Db 386 RTGTSMTSVNWL- - - - -TPNGTLMTHGYSRVIRISVLHDGTLNFTNVTVQD--TGQYTCMV 438
QY 369 QMGQGTRESPTVTPRPSRLTLGIEPVSPTS- - - - -LRVGLQRYLQGS 412
Db 439 TNSAGNTTA- - - - -SATLNVSAVDPAAGGTGSGGGPGSGGGVGGGYTYFT 488
QY 413 SVQLRSRLTYRNLSGDPKRLVTLRLPASLAIEYTVTQLRPNATYSVCVMPLGP- - - - - 465
Db 489 TVTVETLETO- - - - -PGEEA- - - - -LQPRGTBK- - - - -EPPGPTTDGVMG 523
QY 466 -GRVPEGEERACGEAHTPPAVHSNH- - - - -APVTQAREGNL- - - - -PLLIAPAL 507
Db 524 GGRPDAAAGPSSSTTAPAPRSSRPTKAFVPIITDVNTENALKOLDLVNMTKIIIGCFV 583
QY 508 AAVLIAALAAVGAAYCYVRRGR- - - - - - - - - - - - - - - - - - - - - - - - 538
Db 584 AITFWAAVMLV-AFYKLRKQHLKHGHPTRTVEILINVEDELPAASAVSVAASAAVASG 642
QY 539 QVPGAGPLELEGV- - - - -KVPLEPGPKATEGGGEALPSGSECEVPLM 581
Db 643 GVG-GDSHLALPALERDHLNHHVYVAAAFKAHYSSNPGSGCGKGPGLNSIHEPLL 699

RESULT 8
US-11-030-653-38
; Sequence 38, Application US/11030653
; Publication No. US20060147945A1
; GENERAL INFORMATION:
; APPLICANT: Edmonds, Brian
; APPLICANT: Micanovic, Radmila
; APPLICANT: Ou, Weijia
; APPLICANT: Su, Eric
; APPLICANT: Tschang, Sheng-Hung
; APPLICANT: Wang, He
; TITLE OF INVENTION: Novel secreted proteins and their uses
; FILE REFERENCE: X-14001
; CURRENT APPLICATION NUMBER: US/11/030,653
; CURRENT FILING DATE: 2005-01-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-030-653-38

Query Match 10.0%; Score 313.5; DB 7; Length 656;
Best Local Similarity 23.6%; Pred. No. 4.2e-12;
Matches 158; Conservative 79; Mismatches 239; Indels 193; Gaps 27;

QY 19 PGVQCGSPGSCQCS-OPQTVFCTARQTTVPDRVDPDTVGLYVFENGITWLDASSFAGLPG 77
Db 52 PPATSCPACSCSQASRVICTRRDLAEVPASIPVNTRYLNLQENGIOVIRDTDFKHLR 111
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QY	78	LQLDLSONQIASLR-----LPRLLLDLHSHSLALEPGLDTAN-----	118
Db	112	LEILQLSKNLVKIEVGAFNGPLSLNLTLELFNRLTTPVTOAQFEYLSKRLWLNNPPIE 171	
QY	119	-----VVALRLAGLG---LQOLDEGLFSRLRLNLDLSDNQLERVPPVIRGLRG 165	
Db	172	SIPSYAFNRVPSRLRLDGLGELKRLUYISEAAFEGLVNLRYLNLGMCNKDIPNLTAIVR- 230	
QY	166	LTRLRAGNTRIAQLRPEDLAGLA-----ALQELDVSNLSL 201	
Db	231	LEELSLGN-RDULIRPGSFQGLTSRLKWLHMAQVATIERNAFDDLSLELNLSHNNL 289	
QY	202	QALPGDLSGLFPLRLLLAAARNPFCVCLPSWFGFWPVRSHVTLASPBET-----RCHPPP 257	
Db	290	MSLPHDLFTPLHLRLRVLNHNPNHCNDVLMWSWLKET-----VPSNTTCCARCHAPA 344	
QY	258	KNAGRLLELDVADGCGCAPATTTATVTPRVPVREPTALSSSLAFTWLSPT-APATEAPS 316	
Db	345	GLKGRYIGELDQSHFTCYA-----PVIVEP-----PTDLNVTEGMAAELKC 385	
QY	317	PPTAPPTVPVPQDQCPSTCLNGT-----CHLGRHLACLCPGEGTGLY-CES 368	
Db	386	RTGTSMTSVNWL-----TPNGTLMTHGSTRVRIISVLHDGTLNFTNTVQD--TGQYTCMV 438	
QY	369	QMGGTRPSPTFTVTPRPRSLTLGIEPVSPS-----LRVGLQRYLOGS 412	
Db	439	TNSAGNTTA-----SATLNVSAVDPAAGGTGGGGPGGSGGGVGGGYTYFT 488	
QY	413	SVQLRSRLTRYNLSGPKDKRLVTLRLPASLAEYTVTLRPNATYSCVNWPLGP----- 465	
Db	489	TVTVETLETQ-----PGEEA-----LQPRGTEK---EPGPTGTVGWMG 523	
QY	466	-GRVPEGEACGEAHTPPAVHSH-----APVTOAREGNL-----PLLIAPAL 507	
Db	524	GGRPGDAAGPASSSTTAPAPRSRPTKEAFTVPTDVTENALKLDLDVWMKTKIILGCFV 583	
QY	508	AAVLLAALAAGVAAVYCVRRGRAMAAADKQGVGPGAGP---LELBGVKVPLEPGPKATE 564	
Db	584	AITFMAVMVLV-AFYKLRK-----QHQLKHKGHTRTVEIINVEDELPAASAVSV 632	
QY	565	GGGEALPSG 573	
Db	633	AAAAAVASG 641	
RESULT 9			
US-10-486-020-19			
; Sequence 19, Application US/10486020			
; Publication No. US20060127894A1			
; GENERAL INFORMATION:			
; APPLICANT: AZIMZAL, Yalda; BARROSO, Ines;			
; APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;			
; APPLICANT: BOROWSKY, Mark L.; DUGGAN, Brendan M.;			
; APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.;			
; APPLICANT: FORSYTHE, Ian J.; GIETZEN, Kimberly J.;			
; APPLICANT: GORVAD, Ann E.; GRAUL, Richard C.;			
; APPLICANT: GRIFFIN, Jennifer A.; GURURAJAN, Rajagopal;			
; APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;			
; APPLICANT: KABLE, Amy E.; KHAN, Farrah A.;			
; APPLICANT: LEE, Sally;			
; APPLICANT: LEE, Soo Yeun;			
; APPLICANT: LI, Joana X.; REDDY, Roopa;			
; APPLICANT: RICHARDON, Thomas W.; SPRAGUE, William W.;			
; APPLICANT: SWARNAKAR, Anita; TANG, Y. Tom;			
; APPLICANT: WARREN, Bridget A.; XU, Yuming;			
; APPLICANT: YAO, Monique G.; YUE, Henry;			
; APPLICANT: YUE, Huibin			
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH			
; FILE REFERENCE: PP-1126 USN			
; CURRENT APPLICATION NUMBER: US/10/486.020			
; CURRENT FILING DATE: 2004-02-05			
; PRIOR APPLICATION NUMBER: PCT/US02/25465			
; PRIOR FILING DATE: 2002-08-02			
; PRIOR APPLICATION NUMBER: US 60/311,017			

; PRIOR FILING DATE: 2001-08-08			
; PRIOR APPLICATION NUMBER: US 60/313,070			
; PRIOR FILING DATE: 2001-08-17			
; PRIOR APPLICATION NUMBER: US 60/313,071			
; PRIOR FILING DATE: 2001-08-17			
; PRIOR APPLICATION NUMBER: US 60/314,678			
; PRIOR FILING DATE: 2001-08-24			
; PRIOR APPLICATION NUMBER: US 60/316,692			
; PRIOR FILING DATE: 2001-08-31			
; PRIOR APPLICATION NUMBER: US 60/317,913			
; PRIOR FILING DATE: 2001-09-07			
; PRIOR APPLICATION NUMBER: US 60/322,182			
; PRIOR FILING DATE: 2001-09-14			
; PRIOR APPLICATION NUMBER: US 60/340,747			
; PRIOR FILING DATE: 2001-12-07			
; PRIOR APPLICATION NUMBER: US 60/342,761			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 54			
; SOFTWARE: PERL Program			
; SEQ ID NO 19			
; LENGTH: 592			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; OTHER INFORMATION: Incyte ID No: 6803363CD1			
US-10-486-020-19			
Query Match 10.0%; Score 312; DB 6; Length 592;			
Best Local Similarity 25.9%; Pred. No. 4.6e-12;			
Matches 166; Conservative 58; Mismatches 210; Indels 208; Gaps 26;			
QY	2	CSRVPLLPLLLALGPGVQCGPSGCCS-QPQVTFCTARQGTTPRDPVDPDTVGLYVF 60	
Db	3	CWLCVLSPLFLLPAPPPAGGCPARCECTQTRAVACTRRRLTAVPDGIPAEIRLLELS 62	
QY	61	ENGITMLDASSPAGLPGLQLDLSONQIASL-----RLPRLLLDLHSHSLALEPGL 114	
Db	63	RNRIRCLNPGDIALPALEELDLSENAIAHVFPFGAFANLPRLRVGRRLGNQKLIIPGV- 121	
QY	115	DTANVEALRLAGLGQQLDEGLFSRLNLHLDVSDNOLE-RVPPVIRGLRGLTRLAG 173	
Db	122	-----FTRLDNLTLDLSENKLVILLDYTFQDLHSLRRLVEGD 159	
QY	174	NTRIAQLRPEDLAGLAALQELDVSNLSLOALPGDLISGLFPRLRLLLAAARNPFCVPLSW 233	
Db	160	NDLVFVSR-RAFAGULLALEELTLERCNLTALSGESLG--HLRSLGA----- 202	
QY	234	FGPWRESHVTLASPEETRCHFPFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREP 293	
Db	203	----LRLRLHAIASLEDQNFRRLP---GLLHLEID-----NWPLLEEV 238	
QY	294	TALS--SSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQDQCPSTCLNGGTCHLGRH- 351	
Db	239	AAGSLRGLNLTLSVLT--HTNITAVPAAA-----LRHQ 269	
QY	352	-HLACLCPGFTGLYCESQMGQGRPSPTPTPR-----NLSHNPSTVPRGSFRDLVRLRELHLAGALLAVBFOA 313	
Db	270	AHLTCL----- 436	
QY	389	LTIGIEPVSPTSIRVGLQRYLOGSSVQ-----LRSRLTYRNLSGPKRLVTL----- 436	
Db	314	F-LGLRQIRLLNLSNNLLSTLESTFHSVNTLETLRVDGNPLA-CDCLLMIVQRRKTLN 371	
QY	437	---RLPASLAEYTVTQLRPNA-----TVSVCVMP-LGPGRVPEGEACE----- 477	
Db	372	FDGRLPACA---TPAEVRGDALNRLPDSVLFEFVCKPKIKRRLRQRTATAGDVRFL 428	
QY	478	--AHTPPA-----VHSNHAPVTOAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAM 530	
Db	429	CRAEGEPAPTVAMVTPQHRFPVTATSGARARVLPGGTL-----EIQ 468	



QY 531 AAAAQDKGQ---VGPGAGPLEGKVPLEPGPKATEGGGEA 569  
Db 469 DARPODSGTTCVASNAGGNDTYFATLTVRPEPAANRTGEA 510

RESULT 10  
US-11-030-653-14  
; Sequence 14, Application US/11030653  
; Publication No. US20060147945A1  
; GENERAL INFORMATION:  
; APPLICANT: Edmonds, Brian  
; APPLICANT: Micapovic, Radmila  
; APPLICANT: Ou, Weijia  
; APPLICANT: Su, Eric  
; APPLICANT: Tschang, Sheng-Hung  
; APPLICANT: Wang, He  
; TITLE OF INVENTION: Novel secreted proteins and their uses  
; FILE REFERENCE: X-14001  
; CURRENT APPLICATION NUMBER: US/11/030, 653  
; CURRENT FILING DATE: 2005-01-06  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-030-653-14

Query Match 10.0%; Score 312; DB 7; Length 592;  
Best Local Similarity 25.3%; Pred. No. 4.6e-12; Indels 208; Gaps 26;  
Matches 166; Conservative 58; Mismatches 210;  
QY 2 CSRVPLLLPILLALLGPGVGGCPSCQCS-QQTVFCTARQGTTPRDVPPDTVGLYVF 60  
Db 3 CWLCVLSLPLLLPAPPPAGGCPARCECTVQTRAVACTRRITAVDPGIPAEIRLELS 62  
QY 61 ENGITMLDASSFAGLPGQLDLSQNOIASL-----RLPRLLLDLSHNSLLALBPGIL 114  
Db 63 RNRIRCLNPGDLAALPALEBLDLSNAIAHVEPGAFLPRLVRLRGNLQKLIIPGV- 121  
QY 115 DTANVEALRLAGLGLQQLDEGLFSRLNLHLDVSDNOLE-RVPPVIRGLRGLTRLAG 173  
Db 122 -----FRLDNLTLLDSENKVLIDYTFQDLHSRLRLEVG 159  
QY 174 NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLGFLPRLRLAAARNPFCVCLPW 233  
Db 160 NDLVFVSR-RAFAGLALAELETLERCNLTALSGLG---HLRSLG----- 202  
QY 234 FGPWVRESHVTLASPBETRCHFPKKNAGRLLLLELDYADFGCPATTTTATVTPRVVREP 293  
Db 203 ----LRLHLAIASLEQNFRLP---GLLHLBID-----NWPILLEEV 238  
QY 294 TALS-SSLAPTWSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNGGTCHLGRH- 351  
Db 239 AAGSLRGLNLTSLSVT--HTNITAVFAAA-----LRHQ 269  
QY 352 -HLACPEGFTGLYCESQMGQGRSPPTVTPR-----PPRS 388  
Db 270 AHUTCL-----NLSHNPISVTPRGSRFDLVRLEHLAGALLAVVEPQA 313  
QY 389 LTGIEPVPSPSLRVGLQRYLOQSSVQ-----LRSRLTYRNLSPDKRLVTL----- 436  
Db 314 F-LGLRQIRLLNLSNLLSTLESTFHSVNTLETLRVDGNPLA-CDCLLWIVQRKLTN 371  
QY 437 ---RLPASLAEYTVTQLRPNA-----TYSVCVMP-LGPRVPEGEAGE----- 477  
Db 372 FDGRLEPACA---TPAEVRGDALRNLPDSVLFEYFVCKPKIRERLRQRTVATAGEDVRFL 428  
QY 478 --AHTPPA-----VHSNHAHVTOAREGNLPLLIAPALAAVLAALAAVGAAYCVRGRAM 530  
Db 429 CRAEGEPAPTVAVTPOHREVTATTSAGRARVLPGGTL-----EIQ 468  
QY 531 AAAAQDKGQ---VGPGAGPLEGKVPLEPGPKATEGGGEA 569

Db 469 DARPODSGTTCVASNAGGNDTYFATLTVRPEPAANRTGEA 510

RESULT 11  
US-10-196-749-384  
; Sequence 384, Application US/10196749  
; Publication No. US20060094864A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RJC340  
; CURRENT APPLICATION NUMBER: US/10/196, 749  
; CURRENT FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 384  
; LENGTH: 649  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-196-749-384

Query Match 9.9%; Score 309; DB 6; Length 649;  
Best Local Similarity 22.3%; Pred. No. 7.8e-12;  
Matches 141; Conservative 93; Mismatches 214; Indels 184; Gaps 25;  
QY 13 LLLALGP---GVGCPSCQCSQPQTVFCTARQGTTPRDVPPDTVGLYVVFENGITMLDA 69  
Db 17 LFLQVAPLSVMAKSCPSVCRG-DAGFIYCNDRFLTSIPTGIPEDATTLYLQNNQI----- 70  
QY 70 SSFAGLPG-----LQLDLSQNOIASL-----RLPR 95  
Db 71 -NNAGIPSDLKNLLKVERIYLYHNSLDEPPTNLPKYVKLHQLQNNIRTIYDLSLSKIPY 129  
QY 96 LLLLDLSHNSL--LALPGILDTANVEALRLAGLGLQQLDEGLFSRLNLHLDVSDNQL 153  
Db 130 LEEHLDDNSVSAVSIIEGAFRDSNY--LRLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187  
QY 154 ERV-PPVIRGLRGLTRLAGN-----TRIAQLR-----PEDLAG- 187  
Db 188 STISSPSLOGLTKSLRLVDLGNLLNHHGLGDKVFNVLNLTSLVRSNLTAAPVNLPGT 247



QY 188 -----LAALQELDVNSLSQALPGDLSGLFPRLRLAARPNP 225  
 DB 248 NLRKLYLQDNHINRVPNPAFSLRQLYRLDMSNNLSNLPQGFDDLDNITQILRNPNW 307  
 QY 226 NVCPLSWFPGWVRSHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTATVPT 285  
 DB 308 YGCCKMKWRDMLQSLPVKV-NVRGLMCQAPKVRGMAIKDNLNAELFDCCKSGIVSTIQI 366  
 QY 286 TRPVVREPTALSSSLAPT---WLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNG 342  
 DB 367 T-----TAIPNTVYPAQOWPAPVTQKPDINKPKLT----- 397  
 QY 343 GTCHLGRHHLACLCEGFTGLYCESQMGQTRPSTPTVTPRPPRSLTILGIEPVSPSTSLR 402  
 DB 398 -----KQQTGSPS-----RKTTITIVKSVTSDTIH 424  
 QY 403 VGLQRYLGSSVOLRSRLTYRNLSPG-DKRLVTLRLPASLAETVTLQRPNATYSCVM 461  
 DB 425 ISWKALPMTALRLSWLKLGHSPAFGSITETIVT---GERSEYLVTALEPDSPYKVCMV 480  
 QY 462 PLGPGRVPEGE--ACGEAHTPPAVHSHAPVT-----QARE-----GNLPL--LIAPALA 508  
 DB 481 PMETSNLYLFDTPVCITETAPLRMVN--PTTLNREQEKEPYKNPNPLAAIIGGAVA 538  
 QY 509 AVLLAALAAVGAAYCVRGRGMAA--AAQDKGQ 539  
 DB 539 LVTIALLALV-CWYVHRNGSLFRNCAYSKGR 569

RESULT 12  
 US-11-101-316-132  
 ; Sequence 132, Application US/11101316  
 ; Publication No. US20060099657A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID  
 ; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA  
 ; FILE REFERENCE: P3230R1C17C1  
 ; CURRENT APPLICATION NUMBER: US/11/101,316  
 ; CURRENT FILING DATE: 2005-04-06  
 ; PRIOR APPLICATION NUMBER: 10/063526  
 ; PRIOR FILING DATE: 2002-05-03  
 ; PRIOR APPLICATION NUMBER: 10/006867  
 ; PRIOR FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: 09/380137  
 ; PRIOR FILING DATE: 1999-08-25  
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252  
 ; PRIOR FILING DATE: 1999-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087759  
 ; PRIOR FILING DATE: 1998-06-02  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SEQ ID NO 132  
 ; LENGTH: 649  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-11-101-316-132

Query Match 9.9%; Score 309; DB 7; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 7.8e-12;  
 Matches 141; Conservative 93; Mismatches 214; Indels 184; Gaps 25;  
 QY 13 LLLALGP---GVQCPSCGCSQSQPTVCTARQGTTPRDPVDPDTGLYVFENGITMLDA 69  
 DB 17 LFLQVAPLSVMAKSCPSVCRC-DAGFTYCNDRFLTSTGIPEDATTLYLQNNQI----- 70  
 QY 70 SSFAGLPG-----LQLLDLSQNIQIASL-----RLPR 95

DB 71 -NNAGIPSDLKNNLKVERIYLVHNSLDEFPPTNLPKVVKELHQENNIRTTIVDSLSKIPY 129  
 QY 96 LLLLDLSHNSL--LALFPGILDTANVEAIRLAGLGLOQLQDLGFLRRLNLHLDLDVSDNQL 153  
 DB 130 LLELHDDNSVSAVIEGAFRDSNY--LRLFLSRNHLSTIPWGLPRTIEELRLDDNRI 187  
 QY 154 ERV-PPVIRGLRGLRRLRAGN-----TRIAOLR-----PEDLAG- 187  
 DB 188 STISSPSLQGLTSLRKLVLVDGNLNNHGLGDKVFNVLNLTLSLVRNLSLTAAPVNLPGT 247  
 QY 188 -----LAALQELDVNSLSQALPGDLSGLFPRLRLAARPNP 225  
 DB 248 NLRKLYLQDNHINRVPNPAFSLRQLYRLDMSNNLSNLPQGFDDLDNITQILRNPNW 307  
 QY 226 NVCPLSWFPGWVRSHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTATVPT 285  
 DB 308 YGCCKMKWRDMLQSLPVKV-NVRGLMCQAPKVRGMAIKDNLNAELFDCCKSGIVSTIQI 366  
 QY 286 TRPVVREPTALSSSLAPT---WLSPTAPATEAPSPSTAPPTVGPVPOQDCPPSTCLNG 342  
 DB 367 T-----TAIPNTVYPAQOWPAPVTQKPDINKPKLT----- 397  
 QY 343 GTCHLGRHHLACLCEGFTGLYCESQMGQTRPSTPTVTPRPPRSLTILGIEPVSPSTSLR 402  
 DB 398 -----KQQTGSPS-----RKTTITIVKSVTSDTIH 424  
 QY 403 VGLQRYLGSSVOLRSRLTYRNLSPG-DKRLVTLRLPASLAETVTLQRPNATYSCVM 461  
 DB 425 ISWKALPMTALRLSWLKLGHSPAFGSITETIVT---GERSEYLVTALEPDSPYKVCMV 480  
 QY 462 PLGPGRVPEGE--ACGEAHTPPAVHSHAPVT-----QARE-----GNLPL--LIAPALA 508  
 DB 481 PMETSNLYLFDTPVCITETAPLRMVN--PTTLNREQEKEPYKNPNPLAAIIGGAVA 538  
 QY 509 AVLLAALAAVGAAYCVRGRGMAA--AAQDKGQ 539  
 DB 539 LVTIALLALV-CWYVHRNGSLFRNCAYSKGR 569

RESULT 13  
 US-11-376-673-132  
 ; Sequence 132, Application US/11376673  
 ; Publication No. US20060160186A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPRESSED IN STOMACH TUMOR AND  
 ; TITLE OF INVENTION: LUNG TUMOR  
 ; FILE REFERENCE: P3230R1C165C  
 ; CURRENT APPLICATION NUMBER: US/11/376,673  
 ; CURRENT FILING DATE: 2006-03-14  
 ; PRIOR APPLICATION NUMBER: 10/063742  
 ; PRIOR FILING DATE: 2002-05-09  
 ; PRIOR APPLICATION NUMBER: 10/006867  
 ; PRIOR FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: 60/170262  
 ; PRIOR FILING DATE: 1999-12-09  
 ; NUMBER OF SEQ ID NOS: 170  
 ; SEQ ID NO 132  
 ; LENGTH: 649  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-11-376-673-132

Query Match 9.9%; Score 309; DB 7; Length 649;  
 Best Local Similarity 22.3%; Pred. No. 7.8e-12;  
 Matches 141; Conservative 93; Mismatches 214; Indels 184; Gaps 25;



QY 13 LLLALGP---GVQCPSCQCSQPTVFTCAQTGTTVPDRVDPDTVGLYVFPENGITMLDA 69  
Db 17 LFLQVAPLSWMAKSCPSVCR-C-DAGFIYCNDRFLTSIPTGIPEDATFLYLNQNI----- 70  
QY 70 SSFAGLPG-----LQLDLSONQIASL-----RLPR 95  
Db 71 -NNAGIPSLDKNLLKVERIYLYHNSLDEPTNLPKVVKELHQENNIRIITYDLSKIPY 129  
QY 96 LLLLLSHNSL--LALPGILTANVEALRLAGLGLQQLDEGLFSRLRLNHLDLVSDNQL 153  
Db 130 LSELHDDNSVSAVSIEEAGFRDSNY--LRLFLSRNHLSTIPWGLPRTIEBLRDDNRI 187  
QY 154 ERV-PPVIRGLRGLTFLRAGN-----TRIAQLR-----PEDLAG- 187  
Db 188 STISSPSLQGLTSLRLVLNHLNNGHGLGVFFNLVNLTELSELVRNLSLTAAPVNLPGT 247  
QY 188 -----LALQELDVSNLSLQALPGDLGSLGFLPRLRLLAARNPF 225  
Db 248 NLRKLYLDNHINRVPPNFAFYLRLYRLDMNNLSNLPQGFDDLDNITQLILRNPNW 307  
QY 226 NVCPLSWFGPWVRESHVTLASPEETRCHPPKNAGRLLELDYADFGCPATTTTATVPT 285  
Db 308 YGCKMKWVRDLQSLPVKV-NVRGLMCOAPEKVRGMAIKDLNAELFDCCKDSGIVSTIQI 366  
QY 286 TPVVRPTALSSSLAPT---WLSPTAPATEAPSPSTAPPTVGPVPQDCPPSTCLNG 342  
Db 367 T-----TAIPNTVYPAQOMPAPVTKQPDKNPKLT----- 397  
QY 343 GTCHLGRHLACLCPGEGTGLYCESQMGQTRPSPPTVTPRPSRLTLGIEPVSPSRLR 402  
Db 398 -----KQQTGSPS-----RKTIITVKSVTSDTIH 424  
QY 403 VGLQRYLOGSSVQLRSLRLTYRNLGSP-DKRLVTLRLPASLAETVTLQRPNATYSVCVM 461  
Db 425 ISWKALPMTALRLSLWLGHPAFGSITETIVT---GERSEYLVTALEPDSYKVCNV 480  
QY 462 PLGGRVPEEB--ACGEAHTPPAVHSNHPVT-----QARE-----GNLPL--LIAPALA 508  
Db 481 PMETSNLYLDFDETPVICIETETAPLRMYN--PTTTLNREGEKEPKYKPNPLPLAAIIGGAVA 538  
QY 509 AVLLAALAAVGAAYCVRRGRAMAA-AAQDKGQ 539  
Db 539 LVTIALALV-CWYVHRNGSLFSRNCAYSXGR 569

## RESULT 14

US-11-293-697-3826  
; Sequence 3826, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3826  
; LENGTH: 745  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3826

Query Match 9.0%; Score 282.5; DB 7; Length 745;

Best Local Similarity 22.7%; Pred. No. 3.9e-10;  
Matches 171; Conservative 58; Mismatches 254; Indels 271; Gaps 29;

QY 8 LPLPLLLALGPGVQ-CPSGCQCSQP---QTVFCTAROGTTVPDRVDPDTVGLYVFPENG 63  
Db 4 LRALMLVWAL-LGVAGSCPCEACVDKYAHQADCAKRELREVPGLPANVTLSLSANK 62

QY 64 ITMLDASSFAGLPGQLQLDLSONQIASLRLPRLLLLDLSHNSLLALEPGILDTANVEALR 123  
Db 63 ITVLRRGAFADV-----TQVTSW-----LAHNEVRTVEPGAL----- 95  
QY 124 LAGLGLQQLDEGLFSRLRLNHLDLVSDNQLRVP-PVIRGLRGLTFLRAGNTRIAQLRP 182  
Db 96 -----AVLSQLKN-----LDLSHNFISFFPWSDLNLSALQLLKNHN-RLGSLPR 140  
QY 183 EDLAGLALQELDVSNLSLQAL-PGDLGSLGFLPRLRLLAARNPFNCVCLSPFPGPWVRES 241  
Db 141 DALGALPDLRLSRINNRRLRTLAPGTFOAL-SALSHLQLYHNPFFHCGCGLVWLQAWAAS 199  
QY 242 HVTLASPETRCHFPKKNAGRLLLLELDYADFCCPATTTTATVPTTRP----- 288  
Db 200 RVSLEPPDSIACASPPALQGVFVYRLPALPCAPPSVHLSAEPPLPAPGTPPLRAGLAFVLH 259  
QY 289 -----VVREPTALSS-----SL 300  
Db 260 CIADGHPTRLOWLOLQTPGGTVLLEPPVLSGEDDGVGAEEGEGEGDGLLTOTQATPTP 319  
QY 301 APTWLSPTAP-----ATEAPSPPS 319  
Db 320 APAPWAPPATPRFLALANGSLVPLLSAKEAGVYTCRAHNELGANSTSIKRVAAATGPPK 379  
QY 320 TAPPTVGPVPOQDCPP-----STCLNGCTCHLGRHHLACLCPG-----FTGLYCESQMG 371  
Db 380 HAPGAGG---EPDGOAPTSEKSTAKGRNSVLPK-----PEGKIKGOGLKAVSILG 429  
QY 372 QGTRESPTVTPR-----PPRSULTGI 393  
Db 430 E-TETEPEEDTSEGEAEADQILADPAEQRGCGNDPSRVSNHAFNQSAELKPHVPELGV 488  
QY 394 -----EPVSPSTSLRVLQRYLOGSSVQ---LRSRLTYRNLGSPDKRLVTLRLPA 440  
Db 489 TALDVAEREARVQLTFLAARWGPGGAGGAPRGRRLRLLYLCPAGGAAVQWSRVEE 548  
QY 441 SLAETVTLQRPNATYSVCVMPLGPRVPEGEACGEAHTPPAVHSNHPVTQAREGNLP 500  
Db 549 GVNAYWFRGLRGTNYSVCLALAG-----EAC-----HVQVVFSTKKELP 588  
QY 501 LLIAPALAAVLLAALAAV---GAAVCVRRG-----RAMAAAAADK---GGVGP 543  
Db 589 SLIVIVAVSVFLVLVATVPLLGAACHLLAKHPGKPYRLILRPQAPDPMEKRIADFDR 648  
QY 544 AGPLELEGVKVLEPGPKATEGGREALPSGSECE 577  
Db 649 ASYLESE-----KSYPAGGEA--GGREPE 670

## RESULT 15

US-10-196-749-290  
; Sequence 290, Application US/10196749  
; Publication No. US20060094864A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C340  
; CURRENT APPLICATION NUMBER: US/10/196,749  
; CURRENT FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263



```
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 290
; LENGTH: 1523
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-290

Query Match      8.2%; Score 258; DB 6; Length 1523;
Best Local Similarity 25.7%; Pred. No. 2.7e-08;
Matches 94; Conservative 39; Mismatches 115; Indels 118; Gaps 15;

QY 24 CPSCGCSQPQTVFCTARQCTTVPRDVPPTVGLYVFENGITWLDASSFAGLPGLQLLDL 83
Db 725 CPEQCTCME--TVVRCNKGRLALPGMPKDVTELYEGNHLTAV----- 767
QY 84 SQNQIASLRPLRLDLLSHNSLLALEPGILDNTANVEALFAGLGLQQLDEGLFSRLRL 143
Db 768 -PRELSALR--HLTLDLSNNS-----ISMLTNYTFSNMSHL 801
QY 144 HDLDVSDNQLRVP-PVIRGLGLRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQ 202
Db 802 STLILSYNLRICFVHAFNGLSRLVLTLHG-----DISSVPEGSFNDLTSL-- 850
QY 203 ALPGDLGLFRLRLAAARNPNCVPLSWFGPWVRESHVTLASPEETRCHFPKKNAGR 262
Db 851 -----HLALGNPLHDCSLRWLSEWKAGY---KEPGIARCSSPEPMADR 893
QY 263 LLELDYADFGCPATTTTATVTPRVVREPTALSSLAFTWLSPTAPATEAPSP--ST 320
Db 894 LLL-----TTPTHRFOCKGPDVNI-----VAKCNACLSSPCKNN 928
QY 321 APPTVGVPV-----QPDC--PPSTCL-----NGGTCHLGTTRH--LACLCEGF 361
Db 929 GTCTQDFVELYRCACPYSGKDKCTVPINTCIQNPCQHGCTCHLSDSHKGDFSCCP 988
QY 362 TGLYCE 367
Db 989 EGORCE 994
```

Search completed: July 27, 2006, 12:10:26  
Job time : 44 secs



GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: July 27, 2006, 12:03:02 ; Search time 42 Seconds  
(without alignments)  
1369.943 Million cell updates/sec

Title: US-10-677-669-69

Perfect score: 3135

Sequence: 1 MCSRVPLLLPLLLLLALGPG.....PLMGPPGQLOSLHAKPYI 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1500 summaries

Database : PIR 80:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	322	10.3	605	2 JCS239	insulin-like growth
2	302	9.6	605	2 A41915	insulin-like growth
3	282	9.0	626	1 NBHUIA	platelet glycoprot
4	281.5	9.0	603	2 JCI282	insulin-like growth
5	278.5	8.9	603	2 JCI282	insulin-like growth
6	278	8.9	1531	2 T42218	slit-1 protein hom
7	264.5	8.4	420	2 A53531	oncofetal trophobl
8	261	8.3	1523	2 T13953	MEGF5 protein - ra
9	255.5	8.1	1469	2 B36665	slit protein 2 pre
10	255.5	8.1	1480	2 A36665	slit protein 1 pre
11	251	8.0	622	2 JC7973	synleurin - human
12	243.5	7.8	312	1 NBHUIA	leucine-rich alpha
13	240	7.7	560	2 A60164	platelet membrane
14	237	7.6	707	2 JC7763	neutonal leucine-r
15	231	7.4	1025	2 T42626	secreted leucine-r
16	222.5	7.1	536	2 A34901	lysine carboxypept
17	214.5	6.8	1535	2 S46224	peroxidase - frui
18	212.5	6.8	361	2 A53860	chondroadherin pre
19	210.5	6.7	4302	2 A38971	polycystic kidney
20	209	6.7	1091	2 A58532	glial cell membran
21	208.5	6.7	382	2 I39068	proline-arginine-
22	200	6.4	653	2 T25194	hypothetical prote
23	199	6.3	1328	2 T23007	hypothetical prote
24	194.5	6.2	789	2 T28714	hypothetical prote
25	194.5	6.2	1355	2 T28715	hypothetical prote
26	193.5	6.2	421	2 T46266	hypothetical prote
27	193.5	6.2	721	2 E70766	hypothetical prote
28	192.5	6.1	575	2 T29972	hypothetical prote
29	189	6.0	369	2 S20811	proteoglycan I - m

30	189	6.0	369	2	S32793	biglycan precursor
31	189	6.0	839	2	T04859	extensin homolog F
32	188.5	6.0	440	2	A47530	oligodendrocyte-my
33	186	5.9	440	2	A39613	oligodendrocyte-my
34	184	5.9	368	1	BGHUN	biglycan precursor
35	183	5.8	662	2	S42799	garp precursor - h
36	182	5.8	369	2	S32559	biglycan precursor
37	181.5	5.8	357	2	S43317	decorin precursor
38	177.5	5.7	2493	2	A55481	adenylate cyclase
39	176.5	5.6	1495	2	T31434	adenylate cyclase
40	175	5.6	343	2	A41748	denin-180 - rat
41	173	5.5	925	2	JC2033	lumican precursor
42	172.5	5.5	359	1	NBHUC8	G protein-coupled
43	172	5.5	1134	2	T04587	decorin precursor
44	170.5	5.4	2145	2	JC4747	hypothetical prote
45	170	5.4	907	2	JE0176	adenylate cyclase
46	169.5	5.4	760	2	T06291	orphan G protein-c
47	169	5.4	354	2	A55454	extensin homolog T
48	169	5.4	839	2	F75518	decorin precursor
49	168.5	5.4	907	2	JG0193	hypothetical prote
50	167	5.3	800	2	S37387	G protein-coupled
51	167	5.3	1112	2	T10504	intermalin A precu
52	166.5	5.3	549	2	T41744	disease resistance
53	166.5	5.3	800	2	AB1129	hypothetical prote
54	165.5	5.3	360	2	S06280	intermalin A limpo
55	165.5	5.3	526	2	C84552	decorin precursor
56	165.5	5.3	1256	2	S60461	hypothetical prote
57	165.5	5.3	1268	2	A49674	gene flightless-I
58	165	5.3	994	2	H96510	flightless-I homol
59	163.5	5.2	786	2	T01456	probable disease r
60	162	5.2	242	2	T47991	extensin homolog F
61	161	5.1	559	2	T42998	hypothetical prote
62	161	5.1	682	2	A49121	Ras-binding protei
63	161	5.1	682	2	A43318	cell-surface molec
64	160.5	5.1	2910	2	T42214	connectin precurs
65	160	5.1	744	2	E86253	otogelin - mouse
66	159.5	5.1	1112	2	T00952	hypothetical prote
67	159	5.1	572	2	T30947	hypothetical prote
68	159	5.1	613	2	A88684	protein AC7.2 [imp
69	159	5.1	702	2	T21148	hypothetical prote
70	159	5.1	1119	2	AD1822	leucine-rich-repea
71	158.5	5.1	738	2	T19938	hypothetical prote
72	158	5.0	1066	2	T15864	hypothetical prote
73	158	5.0	3570	2	T45025	mucin MUC5B, trach
74	156.5	5.0	360	2	I47020	decorin - rabbit
75	156.5	5.0	980	2	H84632	probable receptor-
76	156	5.0	354	2	S29145	decorin precursor
77	156	5.0	594	2	T23841	hypothetical prote
78	155.5	5.0	903	2	T00705	N-chimerin homolog
79	155.5	5.0	1334	2	T50568	probable multi-dom
80	155	4.9	961	2	T23395	hypothetical prote
81	154.5	4.9	1013	2	T10659	probable serine/th
82	154.5	4.9	1143	2	T10636	hypothetical prote
83	154.5	4.9	1192	2	T48499	receptor-like prot
84	154.5	4.9	1495	2	S60255	transcription co-r
85	153.5	4.9	864	2	T08575	protein kinase hom
86	153.5	4.9	894	1	A41527	protein-tyrosine k
87	153	4.9	699	2	C43674	US4 protein - huma
88	152	4.8	786	2	T08664	Toll protein-like
89	151.5	4.8	695	1	JN0898	follicotropin recept
90	151	4.8	540	2	T12704	leucine-rich prote
91	151	4.8	1389	2	T13852	gene wheeler recept
92	150.5	4.8	695	1	QRHUF	follicotropin recept
93	150.5	4.8	1109	2	T18536	receptor-like prot
94	150	4.8	1134	1	A29944	haoptin precursor
95	149.5	4.8	224	2	T32185	hypothetical prote
96	149.5	4.8	696	2	JC7361	follicotropin recept
97	149	4.8	1025	1	A57676	protein kinase Xa2
98	149	4.8	1143	2	B84431	probable receptor
99	149	4.8	2357	2	A59249	class VII unconven
100	148.5	4.7	375	2	S05390	fibromodulin precu
101	148.5	4.7	610	2	T23836	hypothetical prote
102	148.5	4.7	680	2	T19939	hypothetical prote



103	148.5	4.7	890	2	C96654	hypothetical prote	176	136	4.3	4957	2	T03455	ALR protein - huma
104	148.5	4.7	964	2	T49038	hypothetical prote	177	135.5	4.3	427	2	JC4915	ags protein precu
105	148.5	4.7	1115	2	S40241	G protein-coupled	178	135.5	4.3	499	2	D83333	hypothetical prote
106	148	4.7	338	2	S52284	lumicon, secretory	179	135.5	4.3	1124	2	B84742	probable receptor-
107	148	4.7	1188	2	S49915	extensin-like prot	180	135.5	4.3	5262	2	T03454	ALR protein - huma
108	147.5	4.7	316	2	A11781	proteoglycan-Ib -	181	135	4.3	601	2	S56144	SH3 domain binding
109	147.5	4.7	1385	2	T13987	tlr protein - frui	182	134.5	4.3	613	2	T15489	hypothetical prote
110	147	4.7	1964	2	T09059	notch4 - mouse	183	134.5	4.3	847	2	F96531	hypothetical prote
111	147	4.7	2414	2	A54277	transcription adap	184	134.5	4.3	1039	2	T22117	hypothetical prote
112	146.5	4.7	382	2	T04260	hypothetical prote	185	134	4.3	530	2	A45690	transactivator EBN
113	146.5	4.7	925	2	C84538	probable LRR recep	186	134	4.3	656	2	B47096	hyliB homolog - Str
114	146.5	4.7	1408	2	S16148	gene serrate prote	187	134	4.3	886	2	T40734	probable adenylate
115	146	4.7	369	2	G83434	translocation prot	188	133.5	4.3	277	2	S25770	RSP-1 protein - mo
116	145.5	4.6	380	2	S71876	fibromodulin - chi	189	133.5	4.3	384	2	A41710	promastigote surfa
117	145.5	4.6	886	2	S29605	glycoprotein 350/2	190	133.5	4.3	1068	2	H96769	hypothetical prote
118	145.5	4.6	2142	2	B35098	MHC class III hist	191	133	4.2	576	2	T36729	probable serine/thr
119	145	4.6	458	2	T19941	hypothetical prote	192	133	4.2	852	2	I51259	tyrosine kinase C
120	145	4.6	679	2	T20713	hypothetical prote	193	133	4.2	932	2	T48489	receptor-like prot
121	145	4.6	694	2	JC2237	foliitropin recept	194	133	4.2	1257	2	A88536	protein B0523.5 [i
122	145	4.6	1839	1	OYBYK	adenylate cyclase	195	133	4.2	4391	2	A38096	perlecan precursor
123	144.5	4.6	486	2	B86460	hypothetical prote	196	132.5	4.2	463	1	A36479	milk fat globule m
124	144.5	4.6	2187	2	T30826	nascent polypeptid	197	132.5	4.2	2035	2	A40718	host cell factor C
125	144.5	4.6	3149	1	Q0888	BPLF1 protein - hu	198	132	4.2	3164	1	WNBEH6	UL36 protein - hum
126	144	4.6	695	2	I45896	follicle stimulat	199	131.5	4.2	346	2	T46916	hypothetical prote
127	144	4.6	1019	2	C96519	probable disease r	200	131.5	4.2	890	2	T00800	disease resistance
128	144	4.6	3020	2	A43932	mucin 2 precursor,	201	131.5	4.2	1097	2	A29943	Toll protein precu
129	143.5	4.6	243	2	B41710	promastigote surfa	202	131	4.2	612	2	T10727	protein kinase Xa2
130	143.5	4.6	476	2	T27051	hypothetical prote	203	131	4.2	767	2	B84594	probable LRR recep
131	143.5	4.6	496	2	C96832	hypothetical prote	204	131	4.2	905	2	T00475	probable disease r
132	143.5	4.6	605	2	T50817	protein serine/thr	205	131	4.2	915	2	T09575	smoothelin - human
133	143.5	4.6	683	2	T24486	hypothetical prote	206	131	4.2	1095	2	G96746	hypothetical prote
134	142.5	4.5	1870	2	S37671	MHC class III hist	207	131	4.2	1196	2	T09356	brassinosteroid-in
135	142.5	4.5	1872	2	S36152	MHC class III hist	208	131	4.2	448	2	T27395	hypothetical prote
136	142	4.5	661	2	I56258	RP105 - mouse	209	130.5	4.2	268	2	T19697	hypothetical prote
137	142	4.5	983	2	G84524	probable disease r	210	130	4.1	389	2	H86266	hypothetical prote
138	141.5	4.5	462	2	D84858	hypothetical prote	211	130	4.1	395	2	H75457	hypothetical prote
139	141.5	4.5	836	2	T46070	hypothetical prote	212	130	4.1	768	2	T17462	disease resistance
140	141.5	4.5	1029	2	T05050	protein kinase hom	213	130	4.1	800	2	H84740	proline rich prote
141	141.5	4.5	1051	2	T13174	gp150 protein - fr	214	130	4.1	315	2	T06806	hypothetical prote
142	141	4.5	630	2	AC1129	Internalin B [impo	215	129.5	4.1	780	2	T00366	Notch homolog Motc
143	141	4.5	717	2	T33295	fibromodulin precu	216	129.5	4.1	861	2	A48825	brevican precursor
144	140.5	4.5	376	2	S55275	rsu-1 homolog - hu	217	129.5	4.1	912	2	A54423	protein-tyrosine k
145	140	4.5	277	2	I60122	chitinase [EC 3.2.	218	129.5	4.1	942	2	S23251	procr2 - chicken
146	140	4.5	474	2	S65763	probable LRR recep	219	129.5	4.1	1173	2	I50620	basal transcriptio
147	140	4.5	754	2	A85043	protein kinase hom	220	129.5	4.1	1469	2	T09219	promastigote surfa
148	140	4.5	1029	2	T00712	hypothetical prote	221	129.5	4.1	371	2	S20075	probable disease r
149	139.5	4.4	333	2	T34555	hypothetical prote	222	129	4.1	835	2	T05259	hypothetical prote
150	139.5	4.4	527	2	A75399	probable csp prote	223	129	4.1	910	2	B96770	receptor protein k
151	139.5	4.4	539	2	G70520	MEGF1 protein - ra	224	129	4.1	1027	2	B85089	probable Protein k
152	139.5	4.4	4351	2	T00252	insect-stage-speci	225	129	4.1	1064	2	B86465	hypothetical prote
153	139	4.4	581	2	A45551	hypothetical prote	226	129	4.1	1232	2	T05322	probable receptor-
154	139	4.4	603	2	T24315	hypothetical prote	227	129	4.1	1329	2	C84527	hypothetical prote
155	139	4.4	720	2	T02361	hypothetical prote	228	129	4.1	1342	2	A64828	hypothetical prote
156	139	4.4	1088	2	B86312	FltA6.9 protein -	229	129	4.1	1342	2	E85614	cell division prot
157	139	4.4	2240	2	T37057	probable multi-dom	230	129	4.1	1342	2	G90750	cell division prot
158	138.5	4.4	342	2	A46743	lumican precursor	231	129	4.1	1359	1	AGRT	agrin - rat
159	138.5	4.4	990	2	T14756	hypothetical prote	232	129	4.1	2321	2	S78549	notch3 protein - h
160	138.5	4.4	1650	2	S53457	dominant autoantig	233	128.5	4.1	487	2	A24442	nuclear protein EB
161	138	4.4	630	2	C39930	hypothetical prote	234	128.5	4.1	677	2	H86208	protein F22G5.26 l
162	138	4.4	858	2	T00258	hypothetical prote	235	128.5	4.1	727	2	C84534	hypothetical prote
163	138	4.4	1952	2	T48814	hypothetical prote	236	128.5	4.1	744	2	C84527	probable receptor-
164	137.5	4.4	1151	2	T18535	high molecular mas	237	128.5	4.1	825	2	T29634	hypothetical prote
165	137.5	4.4	4660	2	T42737	gp330 protein prec	238	128.5	4.1	1113	2	T00271	hypothetical prote
166	137	4.4	562	2	T34319	hypothetical prote	239	128.5	4.1	3968	2	A44265	trithorax homolog
167	137	4.4	695	2	JC1493	foliitropin recept	240	128	4.1	597	2	S72468	probable transcrip
168	137	4.4	788	2	AG0786	secreted effector	241	128	4.1	967	2	T48210	hypothetical prote
169	137	4.4	907	1	Q08E21	membrane antigen g	242	128	4.1	1428	2	T08852	lustrin A - Califo
170	137	4.4	4544	1	S02392	alpha-2-macroglobu	243	128	4.1	1914	2	T42535	tenascin Y precurs
171	137	4.4	4545	1	S25111	alpha-2-macroglobu	244	127.5	4.1	1750	2	D86245	hypothetical prote
172	136	4.3	322	2	S72271	proteoglycan Ib pr	245	127.5	4.1	1120	2	B86479	hypothetical prote
173	136	4.3	626	2	A80123	probable antigenic	246	127.5	4.1	1784	2	C96615	hypothetical prote
174	136	4.3	692	2	A34548	foliitropin recept	247	127	4.1	327	2	S20074	promastigote surfa
175	136	4.3	1008	2	D84434	Probable receptor-	248	127	4.1	773	2	T00502	probable receptor-



249	127	4.1	775	1	EDB11	immediate-early pr	322	121.5	3.9	432	2	E96712	unknown protein, 6
250	127	4.1	800	2	G84740	hypothetical prote	323	121.5	3.9	519	2	T07026	ethylene receptor
251	127	4.1	1366	2	T35985	probable large Pro	324	121.5	3.9	635	2	T07794	ethylene receptor
252	127	4.1	1895	2	T06609	disease resistance	325	121.5	3.9	686	2	JC7569	Delta-4 protein -
253	127	4.1	1955	1	AGCH	agrin precursor -	326	121.5	3.9	760	2	JC7569	probable Pto kinase
254	126.5	4.0	268	2	T45616	hypothetical prote	327	121.5	3.9	902	2	T00588	hypothetical prote
255	126.5	4.0	685	2	JC7570	Delta-4 protein -	328	121.5	3.9	1251	2	A57293	latent transformin
256	126.5	4.0	694	2	JC4301	foliitropin recept	329	121.5	3.9	1409	2	T37188	presynaptic activi
257	126.5	4.0	862	2	T46289	hypothetical prote	330	121.5	3.9	2265	1	FNBO	fibronectin - bovi
258	126.5	4.0	999	1	T27756	receptor-like prot	331	121.5	3.9	2297	2	T34918	polyketide synthas
259	126.5	4.0	1091	2	S33596	protein-tyrosine k	332	121.5	3.9	2318	2	A53306	notch 3 protein -
260	126.5	4.0	1777	2	T34369	hypothetical prote	333	121.5	3.9	3530	2	A59266	unconventional myo
261	126	4.0	500	2	S49302	AWJL218 protein -	334	121	3.9	306	2	T52340	cell wall-plasma m
262	126	4.0	865	2	A47282	calcium-binding pr	335	121	3.9	480	2	T00971	probable disease r
263	126	4.0	873	2	A47283	calphotin - fruit	336	121	3.9	485	2	A33647	sulfated disacche
264	126	4.0	996	2	F86410	protein F3M18.12 [	337	121	3.9	733	2	A45301	microtubule-associ
265	126	4.0	1152	2	T31911	hypothetical prote	338	121	3.9	1203	2	A49175	Notch B protein -
266	126	4.0	1820	2	A55494	latent transformin	339	121	3.9	1520	2	T00273	hypothetical prote
267	125.5	4.0	283	2	S13383	hydroxyproline-ric	340	121	3.9	2531	2	S18188	notch protein homo
268	125.5	4.0	548	2	AH1107	internalin H limpo	341	120.5	3.8	299	2	A35272	osteoinductive fac
269	125.5	4.0	635	2	F75477	hypothetical prote	342	120.5	3.8	753	2	JQ0532	OP protein - Kenne
270	125.5	4.0	764	2	A40077	thytotropin recept	343	120.5	3.8	821	2	AB1126	internalin, peptid
271	125.5	4.0	1003	2	T05898	hypothetical prote	344	120.5	3.8	855	2	T17460	disease resistance
272	125	4.0	350	2	S22456	hydroxyproline-ric	345	120.5	3.8	976	2	B46559	probable receptor-
273	125	4.0	476	2	A36478	surface glycoprote	346	120.5	3.8	976	2	T05897	protein kinase hom
274	125	4.0	783	2	T45899	receptor protein k	347	120.5	3.8	981	2	T50851	receptor protein k
275	125	4.0	818	2	F96586	hypothetical prote	348	120.5	3.8	987	2	T50850	receptor protein k
276	125	4.0	991	2	T52400	receptor-like prot	349	120.5	3.8	1118	2	A48292	mucin, tracheobron
277	125	4.0	1504	2	T49896	glycine/proline-ri	350	120.5	3.8	1152	2	A33183	microtubule-associ
278	125	4.0	2026	1	OVBY	adenylate cyclase	351	120.5	3.8	1722	2	E89753	protein FilC7.4 [i
279	124.5	4.0	298	2	B35272	osteoinductive fac	352	120.5	3.8	1778	2	AE1116	internalin protein
280	124.5	4.0	756	2	T27642	hypothetical prote	353	120.5	3.8	3566	1	A40701	tenascin-X precurs
281	124.5	4.0	849	2	G97303	hypothetical prote	354	120	3.8	361	2	AH1469	internalin protein
282	124.5	4.0	910	2	G84648	probable disease r	355	120	3.8	376	2	S15558	probable cell wall
283	124.5	4.0	977	2	C96745	hypothetical prote	356	120	3.8	458	2	T31631	hypothetical prote
284	124.5	4.0	1223	2	E88451	protein K10D2.1 [i	357	120	3.8	892	2	T09071	SH3 domains-contai
285	124.5	4.0	2176	2	T13806	toucan gene protei	358	120	3.8	962	2	T04124	receptor-like prot
286	124	4.0	496	2	D55261	conserved hypotet	359	120	3.8	1126	2	T20801	hypothetical prote
287	124	4.0	543	2	S35047	mucin JUL7 - human	360	120	3.8	1224	2	T40765	webi protein homol
288	124	4.0	574	2	T43556	Wiskott-Aldrich sy	361	119.5	3.8	267	2	S08314	cell wall glycopro
289	124	4.0	605	2	AG0123	probable antigenic	362	119.5	3.8	479	1	A31753	transcription fact
290	124	4.0	729	2	E70803	hypothetical prote	363	119.5	3.8	660	2	T45569	receptor protein k
291	124	4.0	766	2	B85440	receptor kinase-li	364	119.5	3.8	1048	1	XPBEA9	large structural p
292	124	4.0	978	2	E96787	protein T4012.5 [i	365	119.5	3.8	1079	2	C96772	probable receptor
293	124	4.0	1011	2	T45718	receptor-kinase li	366	119.5	3.8	1166	2	F96598	protein F20N2.4 [i
294	124	4.0	1472	2	B54774	ATP binding cassel	367	119.5	3.8	1400	2	B70963	hypothetical prote
295	124	4.0	4135	2	T42629	tenascin-X - bovin	368	119.5	3.8	1596	2	A35927	190K DNA-binding p
296	123.5	3.9	380	2	T01281	probable leucine-r	369	119.5	3.8	1643	2	T14274	versican precursor
297	123.5	3.9	492	2	F86263	hypothetical prote	370	119	3.8	164	2	I33641	mucin 5AC - human
298	123.5	3.9	656	2	AE1479	probable cell surf	371	119	3.8	352	2	S49299	AWJL172 protein -
299	123.5	3.9	690	2	T41296	probable alcohol d	372	119	3.8	424	2	S27783	hypothetical prote
300	123	3.9	528	2	T15198	hypothetical prote	373	119	3.8	550	2	C75557	hypothetical prote
301	123	3.9	574	2	T38819	wiskott-aldrich sy	374	119	3.8	651	2	T42644	hypothetical prote
302	123	3.9	888	2	S23065	ufo protein - mous	375	119	3.8	660	1	QBEB3	BHLF1 protein - hu
303	123	3.9	1072	2	A37127	microtubule-associ	376	119	3.8	808	2	T23129	hypothetical prote
304	123	3.9	2591	2	T30288	pristinamycin I sy	377	119	3.8	864	2	D84740	hypothetical prote
305	122.5	3.9	303	2	S28264	hydroxyproline-xic	378	119	3.8	1006	2	T42731	atrophin-1 relate
306	122.5	3.9	415	2	T13435	hypothetical prote	379	119	3.8	1045	2	T41119	internalin- relate
307	122.5	3.9	592	2	D70863	hypothetical prote	380	118.5	3.8	222	2	H96711	hypothetical prote
308	122.5	3.9	699	2	T05225	extensin homolog F	381	118.5	3.8	400	1	A39822	leukosialin precu
309	122.5	3.9	809	2	B84634	probable receptor-	382	118.5	3.8	677	2	E70722	hypothetical prote
310	122.5	3.9	845	2	T12537	hypothetical prote	383	118.5	3.8	751	2	AC2098	hypothetical prote
311	122.5	3.9	1016	2	T30553	disease resistance	384	118.5	3.8	869	2	A71400	probable disease r
312	122.5	3.9	2944	2	A54849	collagen alpha 1(V	385	118.5	3.8	883	2	S57653	brevican precursor
313	122	3.9	298	2	JC4130	osteoglycin precu	386	118.5	3.8	988	2	T45717	receptor-kinase li
314	122	3.9	326	2	T24722	hypothetical prote	387	118.5	3.8	1173	2	T25893	hypothetical prote
315	122	3.9	596	2	AE1515	internalin like pr	388	118.5	3.8	1356	2	A45445	janusin precursor,
316	122	3.9	623	2	T19876	hypothetical prote	389	118.5	3.8	1607	2	T02837	long chain fatty a
317	122	3.9	672	2	B84782	probable receptor-	390	118	3.8	294	2	T37232	mucin, tracheal (A
318	122	3.9	715	2	G86239	protein F20B24.6 [	391	118	3.8	599	2	T10798	phorophorin-S - Vo
319	122	3.9	719	2	T47727	hypothetical prote	392	118	3.8	667	2	S74254	homeotic protein s
320	122	3.9	921	2	B62334	hypothetical prote	393	118	3.8	823	2	AD1935	general secretion
321	122	3.9	992	2	T05335	hypothetical prote	394	118	3.8	1134	1	JN0711	protein-tyrosine k



395	118	3.8	2471	2	A45128	cell-fate determin
396	117.5	3.7	473	2	D85041	hypothetical prote
397	117.5	3.7	624	2	A55576	collagen alpha 2(X
398	117.5	3.7	660	2	JW0067	chitinase (EC 3.2.
399	117.5	3.7	996	2	T10725	protein kinase Xa2
400	117.5	3.7	1075	2	D70568	hypothetical prote
401	117.5	3.7	1706	2	I84499	zinc finger protei
402	117	3.7	431	2	T27904	hypothetical prote
403	117	3.7	431	2	A46688	hepatocyte growth
404	117	3.7	678	2	JG6707	probable receptor
405	117	3.7	743	2	C84633	probable disease r
406	117	3.7	801	2	T29018	hypothetical prote
407	117	3.7	1007	2	C84668	probable receptor-
408	117	3.7	1009	2	D75399	probable penicilli
409	117	3.7	1328	2	T43060	agrin - electric r
410	117	3.7	1328	2	T30273	hypothetical prote
411	117	3.7	1450	2	T13954	MEGF6 protein - ra
412	117	3.7	1574	2	T37056	probable multi-dom
413	117	3.7	2082	2	T34434	hypothetical prote
414	117	3.7	2232	2	S53363	mucin SAC (clone J
415	116.5	3.7	279	2	S51939	chitinase (EC 3.2.
416	116.5	3.7	439	2	I38467	low density lipopr
417	116.5	3.7	621	2	T27632	hypothetical prote
418	116.5	3.7	794	2	T27633	hypothetical prote
419	116.5	3.7	828	2	A88860	protein ZC518.3 [i
420	116.5	3.7	828	2	T31425	C-terminal domain-
421	116.5	3.7	1048	1	A45344	immediate-early pr
422	116.5	3.7	1446	1	T16199	hypothetical prote
423	116.5	3.7	2229	2	S24169	mucin - rat
424	116	3.7	292	2	S71753	repellent protein
425	116	3.7	652	2	AH2348	hypothetical prote
426	116	3.7	660	2	F86308	Similar to disease
427	116	3.7	729	2	T02565	disease resistance
428	116	3.7	771	2	B97303	hypothetical prote
429	116	3.7	808	2	T07039	Hcr9-0 protein - t
430	116	3.7	845	2	T07039	hypothetical T2 pr
431	116	3.7	907	2	A24938	period protein hom
432	116	3.7	1291	2	T00019	hypothetical prote
433	116	3.7	1494	2	T14355	protein-tyrosine-p
434	116	3.7	1840	2	T30250	G71 protein - mous
435	116	3.7	2531	2	A46019	notch-1 protein -
436	116	3.7	2555	2	A40043	notch protein homo
437	116	3.7	2774	2	A43359	microtubule-associ
438	115.5	3.7	322	2	A53715	apomucin precursor
439	115.5	3.7	513	2	AC3061	hypothetical prote
440	115.5	3.7	513	2	D98225	hypothetical prote
441	115.5	3.7	528	2	I47141	gastric mucin (clo
442	115.5	3.7	696	2	T42659	hypothetical prote
443	115.5	3.7	805	2	T49385	hypothetical prote
444	115.5	3.7	946	2	S27921	nuclear antigen EB
445	115.5	3.7	1093	2	I38533	AF17 protein - hum
446	115.5	3.7	1268	2	S52781	neurocan - mouse
447	115.5	3.7	1460	1	EDB81F	immediate-early pr
448	115.5	3.7	2214	2	T16305	hypothetical prote
449	115.5	3.7	3421	1	WZBE86	367K tegument prot
450	115	3.7	404	2	T08549	hypothetical prote
451	115	3.7	451	2	S74728	hypothetical prote
452	115	3.7	461	2	T10741	extensin-like prot
453	115	3.7	479	1	S22542	transcription fact
454	115	3.7	539	2	AH1216	internalin, probab
455	115	3.7	766	2	T01817	hypothetical prote
456	115	3.7	838	2	T08423	Axin homolog Axil
457	115	3.7	980	2	T05414	protein kinase hom
458	115	3.7	1133	2	E86308	hypothetical prote
459	115	3.7	1220	2	A56136	jagged protein pre
460	115	3.7	2415	1	A39086	aggreacan precursor
461	114.5	3.7	328	2	JQ0985	hydroxyproline-ric
462	114.5	3.7	409	2	T11743	pb47 protein - pig
463	114.5	3.7	505	2	AC1469	internalin like pr
464	114.5	3.7	606	2	T51880	hypothetical prote
465	114.5	3.7	627	2	T27123	hypothetical prote
466	114.5	3.7	638	2	T05606	protein kinase hom
467	114	3.6	218	2	T01104	disease resistance

468	114	3.6	378	2	S00842	leukosialin precur
469	114	3.6	413	1	A34888	transcription fact
470	114	3.6	555	1	S20100	mullerian inhibiti
471	114	3.6	586	2	T29695	hypothetical prote
472	114	3.6	633	2	S62057	proline-rich prote
473	114	3.6	634	2	T00388	hypothetical prote
474	114	3.6	656	2	E75468	hypothetical prote
475	114	3.6	768	2	A42755	p-selectin precurs
476	114	3.6	1290	2	T00018	period protein hom
477	114	3.6	2225	2	T26063	hypothetical prote
478	113.5	3.6	317	2	S53116	mucin (clone PGM-2
479	113.5	3.6	330	2	T46256	brevican - human (
480	113.5	3.6	538	2	T01102	disease resistance
481	113.5	3.6	896	2	B43817	transforming prote
482	113.5	3.6	907	2	A86460	99.9K hypothetical
483	113.5	3.6	938	1	QBEB24	nuclear antigen BB
484	113.5	3.6	1286	2	T33476	hypothetical prote
485	113.5	3.6	1907	2	S50893	protein-tyrosine-p
486	113.5	3.6	2911	2	T05066	hypothetical prote
487	113	3.6	371	2	T49908	hypothetical prote
488	113	3.6	377	2	A48018	mucin 7 precursor,
489	113	3.6	382	2	E84527	hypothetical prote
490	113	3.6	419	2	A90888	hypothetical prote
491	113	3.6	419	2	H85729	hypothetical prote
492	113	3.6	603	2	A75373	probable N-acetyl m
493	113	3.6	979	2	A35913	regulatory factor
494	113	3.6	982	2	A53253	microtubule-associ
495	113	3.6	1002	2	T46033	receptor protein k
496	113	3.6	1025	2	T45647	receptor protein k
497	113	3.6	1069	2	S27922	nuclear antigen EB
498	113	3.6	1247	2	T42209	neural plakophilin
499	113	3.6	1343	2	AF0611	cell division prot
500	113	3.6	2688	2	I49477	alpha-A-crystallin
501	113	3.6	3381	2	T42389	versican precursor
502	112.5	3.6	347	2	S10571	mucin 1 precursor,
503	112.5	3.6	581	2	G96811	unknown protein T1
504	112.5	3.6	731	2	B86369	hypothetical prote
505	112.5	3.6	1075	2	A57377	transcription fact
506	112.5	3.6	1237	2	AC1583	internalin protein
507	112.5	3.6	1680	2	T01367	hypothetical prote
508	112.5	3.6	2479	2	F87386	conserved hypotet
509	112.5	3.6	4006	2	T09070	probable tenascin
510	112	3.6	241	2	S32359	glial growth facto
511	112	3.6	252	2	T01787	thyrotropin recept
512	112	3.6	253	1	JC1319	thyrotropin recept
513	112	3.6	285	2	A41826	probable pheromone
514	112	3.6	383	2	S53716	delta-like homeoti
515	112	3.6	413	2	S48756	transcription fact
516	112	3.6	704	2	AE2107	serine/threonine k
517	112	3.6	731	2	T04455	hypothetical prote
518	112	3.6	742	2	F84643	hypothetical prote
519	112	3.6	764	1	QRHURH	thyrotropin recept
520	112	3.6	883	2	S49126	brevican precursor
521	112	3.6	960	2	G84652	probable receptor-
522	112	3.6	990	2	T03784	hypothetical prote
523	112	3.6	1032	2	T34433	hypothetical prote
524	112	3.6	1289	2	AB2217	hypothetical prote
525	111.5	3.6	224	2	D72861	AcOrf-91 protein -
526	111.5	3.6	383	2	S32975	gene BCRF2 protein
527	111.5	3.6	478	1	I47154	transcription fact
528	111.5	3.6	645	2	T05251	probable disease r
529	111.5	3.6	649	2	T46500	hypothetical prote
530	111.5	3.6	1047	2	A55817	masquerade precurs
531	111.5	3.6	1253	2	T45787	disease resistance
532	111.5	3.6	1298	1	EDBE75	immediate-early pr
533	111.5	3.6	1353	1	JH0675	restriccin precurs
534	111.5	3.6	2649	2	T51023	hypothetical prote
535	111	3.5	274	2	JC8063	heart-restricted l
536	111	3.5	478	2	H86459	hypothetical prote
537	111	3.5	509	2	T05260	probable disease r
538	111	3.5	518	2	S50465	PAC2 protein - yea
539	111	3.5	548	2	E70546	hypothetical prote
540	111	3.5	603	2	S28941	coagulation factor



541	111	3.5	610	2	S35049	mucin JER57 - huma	614	109	3.5	2809	2	T30213	G-cadherin - sea u
542	111	3.5	620	2	T50150	yeast nrd1-like pr	615	108.5	3.5	308	2	JC7125	epidermal growth f
543	111	3.5	699	1	QRHUUT	lutropin-choriogon	616	108.5	3.5	389	2	S27200	proline-rich prote
544	111	3.5	853	2	T17461	disease resistance	617	108.5	3.5	402	2	A84581	probable disease r
545	111	3.5	932	2	T21338	hypothetical prote	618	108.5	3.5	418	2	T15142	hypothetical prote
546	111	3.5	984	2	T48216	hypothetical prote	619	108.5	3.5	499	2	A11107	internatin E limpo
547	111	3.5	1721	1	I38902	retinoblastoma bin	620	108.5	3.5	514	2	H70699	probable ppp prote
548	111	3.5	2524	2	A35844	Xotch protein - Af	621	108.5	3.5	548	1	I37577	islet cell antigen
549	110.5	3.5	359	2	C55066	tyrosine decarboxy	622	108.5	3.5	662	2	A45155	mucin FIM-C.1 - Af
550	110.5	3.5	421	2	A60058	neural cell adhesi	623	108.5	3.5	698	2	I39713	celB protein - Agr
551	110.5	3.5	512	2	G86459	Hypothetical 55.6	624	108.5	3.5	710	1	Q0BE22	membrane antigen g
552	110.5	3.5	525	1	A58674	neutrotrophin-3 rec	625	108.5	3.5	740	2	B84741	hypothetical prote
553	110.5	3.5	533	2	T07970	aromatic-L-amino-a	626	108.5	3.5	756	2	G86308	Similar to disease
554	110.5	3.5	565	2	J00338	Frizzled-2 protein	627	108.5	3.5	764	2	A35956	thyrotropin recept
555	110.5	3.5	684	2	T01267	leucine-rich repea	628	108.5	3.5	783	1	A38637	Ras interactor RIN
556	110.5	3.5	803	1	S35695	neutrotrophin-3 rec	629	108.5	3.5	825	1	A40026	neutrotrophin-3 rec
557	110.5	3.5	815	2	B56708	extracellular sign	630	108.5	3.5	855	2	C82983	hypothetical prote
558	110.5	3.5	855	2	T07015	Cf-4A protein - to	631	108.5	3.5	1011	2	C84524	probable disease r
559	110.5	3.5	972	2	S33015	hypothetical prote	632	108.5	3.5	1125	2	B41206	microtubule-associ
560	110.5	3.5	992	2	A31666	hypothetical prote	633	108.5	3.5	1176	2	T49482	hypothetical prote
561	110.5	3.5	1207	2	T00378	KIAA0641 protein -	634	108.5	3.5	1184	2	G01763	atrophin-1 - human
562	110.5	3.5	1295	2	A32901	glp1 protein precu	635	108.5	3.5	1344	1	A35175	mucin 1 precursor,
563	110.5	3.5	1344	2	T14316	rig-1 protein - mo	636	108.5	3.5	1357	2	T29265	hypothetical prote
564	110.5	3.5	1346	2	T17412	polyketide synthas	637	108.5	3.5	1487	2	T02850	hypothetical prote
565	110.5	3.5	1736	2	T00391	hypothetical prote	638	108.5	3.5	3707	2	S18252	heparan sulfate pr
566	110.5	3.5	2476	2	T34022	zonadhesin - pig	639	108	3.4	348	2	JQ0431	flagellar hook-len
567	110	3.5	275	2	T51437	hypothetical prote	640	108	3.4	409	2	AG0752	glycoprotein C - h
568	110	3.5	391	2	T04609	hypothetical prote	641	108	3.4	511	1	VGBE1K	chitinase (EC 3.2.
569	110	3.5	549	2	S32987	hypothetical prote	642	108	3.4	542	2	I39540	proline-rich prote
570	110	3.5	691	2	D84889	probable receptor-	643	108	3.4	544	2	T17547	probable disease r
571	110	3.5	708	2	D96711	hypothetical prote	644	108	3.4	550	2	T36746	microtubule-associ
572	110	3.5	719	2	T02154	protein kinase hom	645	108	3.4	638	1	XXAV	hypothetical prote
573	110	3.5	764	2	I48882	thyrotropin recept	646	108	3.4	741	2	T05250	proteobacterae S
574	110	3.5	846	2	H70599	hypothetical prote	647	108	3.4	862	2	S43922	probable disease r
575	110	3.5	846	2	T21700	hypothetical prote	648	108	3.4	996	2	JE0237	versican - pig-tai
576	110	3.5	951	2	A96770	hypothetical prote	649	108	3.4	1017	2	T31354	apolipoprotein E r
577	110	3.5	1123	2	D96756	receptor-like prot	650	108	3.4	1217	2	T51140	probable potassium
578	110	3.5	1483	2	E86143	F6F3.12 protein -	651	108	3.4	1217	2	T51141	disease resistance
579	110	3.5	1711	1	A55148	protein-tyrosine-p	652	108	3.4	2783	1	A41948	alpha-fetoprotein
580	110	3.5	2703	1	A24420	notch protein - fr	653	108	3.4	3511	2	A59295	unconventional myo
581	110	3.5	2715	2	T13049	eyelid - fruit fly	654	108	3.4	4613	2	T17409	polyketide synthas
582	110	3.5	3942	2	T42730	Bassoon protein -	655	108	3.4	7576	2	T17428	FK506 polyketide s
583	109.5	3.5	219	2	A86228	hypothetical prote	656	107.5	3.4	363	2	H87702	hypothetical prote
584	109.5	3.5	273	2	T10361	hypothetical prote	657	107.5	3.4	369	2	S20500	hydroxyproline-ric
585	109.5	3.5	318	2	T29479	hypothetical prote	658	107.5	3.4	417	2	C96770	hypothetical prote
586	109.5	3.5	428	2	E71415	probable coll wall	659	107.5	3.4	427	2	S74211	PAS-6/7 protein pr
587	109.5	3.5	473	2	S36553	I2 protein - human	660	107.5	3.4	536	2	H71563	hypothetical prote
588	109.5	3.5	507	2	T44768	antifreeze glycope	661	107.5	3.4	604	2	S25203	srmr protein - Str
589	109.5	3.5	538	2	S57459	hook-containing pr	662	107.5	3.4	655	2	G96524	protein Tln15.9 [1
590	109.5	3.5	558	2	JCS878	plasma hyaluronan-	663	107.5	3.4	832	2	A31246	neurogenic protein
591	109.5	3.5	583	1	S22544	transcription fact	664	107.5	3.4	880	2	S00670	cellulose synthase
592	109.5	3.5	612	2	I73633	gene trkC protein	665	107.5	3.4	881	2	B98320	receptor kinase-li
593	109.5	3.5	825	2	A55178	neutrotrophin recep	666	107.5	3.4	1009	2	T45645	tumor suppressor p
594	109.5	3.5	839	1	I73632	neutrotrophin-3 rec	667	107.5	3.4	1099	2	A56155	formin isoform IV
595	109.5	3.5	874	2	E97302	hypothetical prote	668	107.5	3.4	1206	2	S24407	DNA-binding protei
596	109.5	3.5	878	2	T21621	hypothetical prote	669	107.5	3.4	1324	2	S52863	formin - mouse
597	109.5	3.5	954	2	T19765	hypothetical prote	670	107.5	3.4	1468	2	T11515	tegument protein 2
598	109.5	3.5	1299	2	T47182	hypothetical prote	671	107.5	3.4	3534	2	T42567	platelet glycoprot
599	109.5	3.5	1776	1	RRWPYM	genome polypeptin	672	107	3.4	176	1	A46606	extensin-like prot
600	109.5	3.5	2531	2	T31070	notch homolog - se	673	107	3.4	228	2	S23504	fibronectin - chic
601	109.5	3.5	2717	2	A43203	DNA-binding protei	674	107	3.4	273	2	A28512	transmembrane gly
602	109	3.5	379	2	T05441	proline-rich prote	675	107	3.4	354	2	A48931	infected cell prot
603	109	3.5	379	2	D85257	extensin-like prot	676	107	3.4	358	1	WMBE38	dermal gland prote
604	109	3.5	395	2	I52842	CD43 Lp-3 antigen	677	107	3.4	416	1	SKXLAG	mucin - rat (fragm
605	109	3.5	395	2	A43545	leukostalin CD43 p	678	107	3.4	447	2	A39321	transcription fact
606	109	3.5	403	2	S52796	prp12 protein - hu	679	107	3.4	452	2	C41602	hypothetical prote
607	109	3.5	426	2	JQ1696	pistil extensin-11	680	107	3.4	518	2	F75460	coagulation factor
608	109	3.5	431	2	T04868	hypothetical prote	681	107	3.4	615	1	KFHU12	dysglycogen alpha
609	109	3.5	437	2	A54595	transcription fact	682	107	3.4	650	1	S59630	phermone response
610	109	3.5	498	2	C96756	receptor-like prot	683	107	3.4	840	1	S69204	hypothetical prote
611	109	3.5	613	2	T42671	hypothetical prote	684	107	3.4	915	2	T12526	structural polypro
612	109	3.5	833	2	S19087	gene Delta protein	685	107	3.4	1063	1	GNWVR4	osteonidogen - hum
613	109	3.5	1611	2	T38236	hypothetical prote	686	107	3.4	1376	2	G00043	



687	107	3.4	1389	2	I58157	periaxin - rat	760	105	3.3	1133	2	A54164	sterol regulatory
688	107	3.4	2723	2	T03221	probable polyketid	761	105	3.3	1135	2	T30561	Scythe protein - A
689	107	3.4	7463	2	T36248	CDA peptide synthe	762	105	3.3	1136	1	S57845	protein-tyrosine k
690	106.5	3.4	304	2	A42993	transcription fact	763	105	3.3	1456	2	T01397	LTR gag/pol polypr
691	106.5	3.4	353	2	A41558	N-synde can - rat (	764	105	3.3	1658	2	D75489	hypothetical prote
692	106.5	3.4	505	2	B46629	mucin 6, gastric (	765	105	3.3	1844	2	S01956	hypothetical prote
693	106.5	3.4	509	2	D86911	conserved hypothet	766	105	3.3	2133	2	T30637	hypothetical prote
694	106.5	3.4	509	2	T10013	probable phosphopr	767	105	3.3	2133	2	A50979	vesicular precursor
695	106.5	3.4	517	2	AD1570	internalin, probab	768	105	3.3	2769	1	UIBO	thyroglobulin prec
696	106.5	3.4	620	2	S06733	hydroxyproline-ric	769	104.5	3.3	329	2	T17033	leucine rich repea
697	106.5	3.4	827	2	A23963	cellB protein (limp	770	104.5	3.3	407	2	C70816	hypothetical prote
698	106.5	3.4	925	2	H96638	protein TIF9.20 li	771	104.5	3.3	464	2	T35943	probable hydrolyti
699	106.5	3.4	998	2	C75489	conserved hypothet	772	104.5	3.3	530	2	T32812	hypothetical prote
700	106.5	3.4	1003	2	T13856	ksr protein - frui	773	104.5	3.3	639	2	G02919	transcription fact
701	106.5	3.4	1161	2	S57180	probable membrane	774	104.5	3.3	662	2	T04856	hypothetical prote
702	106.5	3.4	1184	2	S08332	atrophin-1 - human	775	104.5	3.3	700	2	A42395	luteolin receptor
703	106.5	3.4	1305	2	AB0168	probable cell divi	776	104.5	3.3	707	1	A34458	gelatinase B (EC 3
704	106.5	3.4	1442	2	T42607	transcription acti	777	104.5	3.3	707	1	A53796	gelatinase B (EC 3
705	106.5	3.4	1892	2	T18314	hypothetical prote	778	104.5	3.3	744	2	T35192	probable ABC trans
706	106.5	3.4	2090	2	S26058	hypothetical prote	779	104.5	3.3	755	2	T20950	hypothetical prote
707	106.5	3.4	2453	2	S60254	probable transform	780	104.5	3.3	909	1	QRXLL1	LDL receptor 1 pre
708	106	3.4	135	2	T43996	nuclear receptor c	781	104.5	3.3	960	1	S28262	kinesin-related pr
709	106	3.4	167	2	A33532	AtAGP4 - Arabidops	782	104.5	3.3	1117	2	JC4934	delta-crystallin/E
710	106	3.4	216	2	I51920	mucin SMUC-40 - hu	783	104.5	3.3	1194	2	E96624	hypothetical prote
711	106	3.4	287	2	S65765	nucin - rhesus mac	784	104.5	3.3	1241	2	T37190	nephlin - human
712	106	3.4	405	2	S78691	chitinase (EC 3.2.	785	104.5	3.3	1505	2	JC4851	hypoxia-inducible
713	106	3.4	431	2	S47538	flagellar hook-len	786	104.5	3.3	1851	2	T19964	hypothetical prote
714	106	3.4	435	2	S47538	acrosin (EC 3.4.21	787	104.5	3.3	1898	2	S46216	leukocyte antigen-
715	106	3.4	443	2	A24993	transcription fact	788	104.5	3.3	2117	2	T36180	CDA peptide synthe
716	106	3.4	449	2	A45977	transcription fact	789	104	3.3	232	2	A60095	larval glue protei
717	106	3.4	567	2	D48613	cellulase (EC 3.2.	790	104	3.3	306	2	I49139	lymphotoxin-beta -
718	106	3.4	666	2	B70803	gab geranylgeranyl	791	104	3.3	318	2	B64900	hypothetical prote
719	106	3.4	701	2	D48613	hypothetical prote	792	104	3.3	326	2	A46676	CD68 homolog macro
720	106	3.4	818	2	T01105	gab polyprotein -	793	104	3.3	332	2	S43988	protein phosphatas
721	106	3.4	822	2	T51049	disease resistance	794	104	3.3	360	2	S68209	sds22 protein homo
722	106	3.4	850	2	S56015	related to nucleol	795	104	3.3	365	2	A39481	serum response fac
723	106	3.4	901	2	A49227	gastric mucin MUC5	796	104	3.3	426	2	D88103	protein W10G11.6 f
724	106	3.4	914	2	T17233	sialidase - Actino	797	104	3.3	440	2	I49681	glyceroldehyde-3-p
725	106	3.4	1064	2	A40136	hypothetical prote	798	104	3.3	470	2	S46536	L2 protein - human
726	106	3.4	1603	2	A48613	fibropellin Ia - s	799	104	3.3	537	2	A46611	myosin-binding pro
727	106	3.4	1958	2	B40505	gag/pol polyprotei	800	104	3.3	538	2	S65764	chitinase (EC 3.2.
728	106	3.4	2554	1	TVFF7L	hypothetical prote	801	104	3.3	593	2	S49525	glycoprotein G - s
729	106	3.4	3938	2	T42761	kinase-related pro	802	104	3.3	712	1	I46031	gelatinase B (EC 3
730	105.5	3.4	395	2	T01392	Bassoon protein -	803	104	3.3	895	2	S20582	dystrophin-associa
731	105.5	3.4	486	2	A41537	leucine-rich repea	804	104	3.3	927	2	T24031	hypothetical prote
732	105.5	3.4	510	2	A42750	DNA-binding protei	805	104	3.3	1045	2	T16275	hypothetical prote
733	105.5	3.4	668	2	T05257	insulinoma-associa	806	104	3.3	1547	2	T28657	blackjack protein,
734	105.5	3.4	688	2	T04568	probable disease r	807	104	3.3	1575	2	S68448	synaptotagmin, 170K
735	105.5	3.4	695	2	S62400	protein kinase hom	808	104	3.3	1711	2	T31337	1,4-beta-glucanase
736	105.5	3.4	772	2	T13078	amphiphysin (Clone	809	104	3.3	1744	2	A54370	tensin, cardiac mu
737	105.5	3.4	780	2	A48143	HF-1 regulatory el	810	104	3.3	3507	2	T34513	hypothetical prote
738	105.5	3.4	952	2	S32954	hypothetical prote	811	103.5	3.3	206	1	NBHUIB	platelet glycoprot
739	105.5	3.4	1132	2	A35098	MHC class III hist	812	103.5	3.3	264	2	PQ0478	pistil extensin-li
740	105.5	3.4	1172	2	T00065	hypothetical prote	813	103.5	3.3	281	2	D70845	hypothetical prote
741	105.5	3.4	1621	2	T15264	hypothetical prote	814	103.5	3.3	333	2	PQ0479	pistil extensin-li
742	105.5	3.4	1712	2	A38261	masking protein pr	815	103.5	3.3	411	1	I55604	platelet glycoprot
743	105.5	3.4	1839	1	RRWPM	genome polyprotein	816	103.5	3.3	419	2	T49292	hypothetical prote
744	105.5	3.4	2477	2	S14428	fibronectin precur	817	103.5	3.3	444	1	A39794	transcription fact
745	105.5	3.4	3033	1	QJ01303	genome polyprotein	818	103.5	3.3	489	2	F75591	p49 secreted prote
746	105	3.3	349	2	T05857	hypothetical prote	819	103.5	3.3	625	2	A26456	nicotinic acetylch
747	105	3.3	422	2	I37891	hypothetical prote	820	103.5	3.3	654	2	T33044	hypothetical prote
748	105	3.3	454	2	E75291	interleukin-11 rec	821	103.5	3.3	889	2	T20123	hypothetical prote
749	105	3.3	460	2	T33110	probable cell wall	822	103.5	3.3	889	2	T00353	hypothetical prote
750	105	3.3	486	1	A57601	hypothetical prote	823	103.5	3.3	975	2	I48974	hypothetical prote
751	105	3.3	511	1	VBBER4	transcription fact	824	103.5	3.3	980	2	S54986	receptor-protein t
752	105	3.3	566	2	T34842	glycoprotein C - h	825	103.5	3.3	1020	2	A29355	fibronectin - chic
753	105	3.3	620	2	A70525	probable transferr	826	103.5	3.3	1144	2	A54810	TMV resistance pro
754	105	3.3	658	2	T08153	hypothetical prote	827	103.5	3.3	1171	2	T35548	hypothetical prote
755	105	3.3	730	2	JC1456	cysteine proteinas	828	103.5	3.3	1268	2	T31420	C-terminal domain-
756	105	3.3	764	2	JC5643	gelatinase B (EC 3	829	103.5	3.3	1590	2	B86398	protein TN9.24 fi
757	105	3.3	847	1	A33800	thyroid stimulat	830	103.5	3.3	1603	2	S23810	collagen alpha 1(X
758	105	3.3	895	2	I54343	mixed-lineage prot	831	103.5	3.3	1638	2	A42091	transcription acti
759	105	3.3	976	2	A36355	dystroglycan - hum	832	103.5	3.3				



833	103.5	3.3	1733	1	B45344	probable nuclear a	906	102	3.3	567	2	JC5538	Rab geranylgeranyl
834	103.5	3.3	3739	2	T17410	polyketide synthas	907	102	3.3	585	1	B70747	probable serine/th
835	103	3.3	168	2	S52994	arabinogalactan-li	908	102	3.3	650	2	B87791	protein B0207.1 li
836	103	3.3	191	2	E84740	hypothetical prote	909	102	3.3	670	2	T22293	zinc finger protei
837	103	3.3	227	2	T27905	hypothetical prote	910	102	3.3	715	2	T12534	hypothetical prote
838	103	3.3	263	2	S01360	salivary glue prot	911	102	3.3	722	2	I48324	DELTA-like 1 mou
839	103	3.3	362	2	A44083	meq protein - Mare	912	102	3.3	728	2	D86278	hypothetical prote
840	103	3.3	367	2	AC1328	internalin protein	913	102	3.3	890	2	E84846	hypothetical recep
841	103	3.3	379	2	T16213	APX-1 protein homo	914	102	3.3	896	1	A35782	cytokine receptor
842	103	3.3	394	2	C84905	probable extensin	915	102	3.3	923	2	A39596	progestrone recep
843	103	3.3	515	2	F70904	hypothetical prote	916	102	3.3	963	2	A55926	DNA binding protei
844	103	3.3	535	1	S76953	protein kinase (EC	917	102	3.3	1008	2	T04462	hypothetical prote
845	103	3.3	550	2	G70597	probable proteinas	918	102	3.3	1021	2	H75423	hypothetical prote
846	103	3.3	575	2	JG0181	Kill2 protein - hu	919	102	3.3	1032	2	D83637	serine/threonine p
847	103	3.3	611	2	B86387	unknown protein (i	920	102	3.3	1052	2	B49120	protein-tyrosine k
848	103	3.3	648	2	T35120	hypothetical prote	921	102	3.3	1069	2	D85383	hypothetical prote
849	103	3.3	701	2	F48613	gag polyprotein -	922	102	3.3	1137	2	A86335	T20H2.9 protein -
850	103	3.3	793	2	JC7390	thyroid stimulatn	923	102	3.3	1166	2	T13958	syncAP-bl protein
851	103	3.3	799	1	TVRTTB	nerve growth facto	924	102	3.3	1249	2	T14270	Ras-GTPase activat
852	103	3.3	813	2	T04313	protein kinase Xa2	925	102	3.3	1293	2	T14259	ras GTPase-activat
853	103	3.3	851	2	S67285	NUD1 protein - yea	926	102	3.3	1692	2	A33988	adenylate cyclase
854	103	3.3	863	2	A55173	cf-9 protein precu	927	102	3.3	1985	2	S19151	hypothetical prote
855	103	3.3	915	2	S36327	clathrin assembly	928	102	3.3	2218	2	B84683	hypothetical prote
856	103	3.3	1040	2	T29092	TSC-22 protein hom	929	102	3.3	2437	2	S42612	transmembrane prot
857	103	3.3	1121	2	A82809	exodeoxyribonuclea	930	102	3.3	2440	2	S39162	transcription coac
858	103	3.3	1199	2	A40670	nuclear envelope p	931	102	3.3	2441	2	S39161	CREB-binding prote
859	103	3.3	1201	2	G86441	unknown protein (i	932	102	3.3	3124	2	A40020	collagen alpha 1(X
860	103	3.3	1275	2	T33369	hypothetical prote	933	102	3.3	5147	1	IJFPTM	cadherin-related t
861	103	3.3	1340	2	A39808	proteoglycan core	934	101.5	3.2	98	2	S53367	mucin SAC (clone M
862	103	3.3	1541	2	T02831	AAA protein f4171.	935	101.5	3.2	173	2	T47176	hypothetical prote
863	103	3.3	1894	2	C54689	protein-tyrosine-p	936	101.5	3.2	244	2	A40428	nonspecific cross-
864	103	3.3	2207	1	GNNY5P	genome polyprotein	937	101.5	3.2	372	2	T29359	hypothetical prote
865	103	3.3	2481	2	A43908	fibronectin - Afri	938	101.5	3.2	409	2	T43599	yop targeted effec
866	103	3.3	3133	2	S52093	hemocytin - silkw	939	101.5	3.2	547	2	B56573	nuclear pore compl
867	102.5	3.3	217	2	S01358	salivary glue prot	940	101.5	3.2	654	2	C87587	hypothetical prote
868	102.5	3.3	252	2	T04739	hypothetical prote	941	101.5	3.2	657	2	B84869	probable Sfl6 prot
869	102.5	3.3	316	2	T31880	hypothetical prote	942	101.5	3.2	710	2	T44753	hypothetical prote
870	102.5	3.3	338	2	I53043	transforming prote	943	101.5	3.2	728	2	I50719	C-Delta-1 - chicke
871	102.5	3.3	352	2	S17313	transcription fact	944	101.5	3.2	733	2	A87168	conserved hypotet
872	102.5	3.3	371	2	F70555	hypothetical prote	945	101.5	3.2	833	2	AF2089	hypothetical prote
873	102.5	3.3	379	2	S31719	proline-rich prote	946	101.5	3.2	869	2	A55384	transcription fact
874	102.5	3.3	383	2	B86272	protein F16A14.12	947	101.5	3.2	921	2	S40495	collagen alpha 1(I
875	102.5	3.3	385	2	S53718	homeotic protein d	948	101.5	3.2	947	2	G86420	probable receptor-
876	102.5	3.3	385	2	A54785	preadipocyte facto	949	101.5	3.2	977	2	I52657	seizure-related pr
877	102.5	3.3	421	2	T30709	core protein homol	950	101.5	3.2	984	1	A34076	protein-tyrosine k
878	102.5	3.3	507	1	A32385	erythropoietin rec	951	101.5	3.2	1034	2	JC5569	serine proteinase
879	102.5	3.3	627	2	D75393	serine proteinase,	952	101.5	3.2	1039	2	A85096	hypothetical prote
880	102.5	3.3	674	2	T05264	probable serine/ch	953	101.5	3.2	1429	2	S06434	homeotic protein 1
881	102.5	3.3	706	2	S04411	synapsin Ia - bovi	954	101.5	3.2	1668	2	T13748	sex comb protein -
882	102.5	3.3	730	1	I52580	gelatinase B (EC 3	955	101.5	3.2	1733	2	S27939	tensin - chicken
883	102.5	3.3	760	1	S07896	transcription fact	956	101.5	3.2	4543	1	A53102	alpha-2-macroglobu
884	102.5	3.3	904	2	T46170	disease resistance	957	101	3.2	240	2	B24264	proline-rich prote
885	102.5	3.3	907	2	E96636	hypothetical prote	958	101	3.2	249	2	S72619	hypothetical prote
886	102.5	3.3	942	1	JQ1674	protein kinase TWK	959	101	3.2	294	2	T34537	hypothetical prote
887	102.5	3.3	964	2	JC5545	integrin beta-4 pr	960	101	3.2	360	2	S25561	transcription fact
888	102.5	3.3	1013	2	A46422	hypothetical prote	961	101	3.2	373	2	A44478	probable cell grow
889	102.5	3.3	1115	1	IJMSNL	neural cell adhesi	962	101	3.2	401	2	A48423	engrailed homeodom
890	102.5	3.3	1233	2	T15316	hypothetical prote	963	101	3.2	482	2	A44997	mezoquite houseom
891	102.5	3.3	1350	2	S36793	hypothetical prote	964	101	3.2	492	2	B86911	probable penicilli
892	102.5	3.3	1367	1	S48478	glucan 1,4-alpha-g	965	101	3.2	574	2	B87619	sensor histidine k
893	102.5	3.3	1678	2	T35547	hypothetical prote	966	101	3.2	610	2	A28798	myosin-light-chain
894	102.5	3.3	1779	2	T31085	xylanase - Caldice	967	101	3.2	613	2	A40497	dihydrolipoamide S
895	102.5	3.3	1813	2	T30564	resistance protein	968	101	3.2	615	1	XXHU	dihydrolipoamide S
896	102.5	3.3	1863	2	S46217	protein-tyrosine-p	969	101	3.2	628	2	JQ0110	hypothetical 69K p
897	102.5	3.3	1875	2	A36429	integrin beta-4 ch	970	101	3.2	671	2	D84648	probable disease r
898	102.5	3.3	2207	2	S09553	genome polyprotein	971	101	3.2	688	2	T18263	S-layer protein -
899	102	3.3	301	2	JQ1663	hybrid proline-ric	972	101	3.2	700	2	D70951	probable UvrD - My
900	102	3.3	307	2	S36779	ribosome-binding p	973	101	3.2	739	2	I56187	transcription fact
901	102	3.3	317	2	A28996	proline-rich prote	974	101	3.2	796	2	T21460	hypothetical prote
902	102	3.3	353	2	B36963	bcsA 5'-region pro	975	101	3.2	846	1	QOBE03	HOR1 protein - hu
903	102	3.3	413	2	T49545	hypothetical prote	976	101	3.2	1043	2	A56037	DNA-binding protei
904	102	3.3	532	2	S74453	hypothetical prote	977	101	3.2	1127	2	T32404	hypothetical prote
905	102	3.3	554	1	FQHUMP	macrophage colony-	978	101	3.2	1257	2	S28764	neurocan precursor



979	101	3.2	1367	2	T33819	hypothenical prote	1052	99.5	3.2	352	2	S05500	Ig alpha-1 chain C
980	101	3.2	1513	2	A54895	mucin 2, intestina	1053	99.5	3.2	353	1	AIHU	Ig alpha-1 chain C
981	101	3.2	1792	2	A57075	tensin - chicken	1054	99.5	3.2	353	2	S36438	EBP protein - hyd
982	101	3.2	2946	2	T15840	hypothenical prote	1055	99.5	3.2	375	1	TDHUN4	monocyte surface g
983	101	3.2	3176	2	CGH3A	collagen alpha 3(V	1056	99.5	3.2	383	1	VBEBKG	glycoprotein precu
984	100.5	3.2	138	2	D96715	protein F4N2.10 (I	1057	99.5	3.2	387	2	B49175	Motch A protein -
985	100.5	3.2	262	2	T33408	hypothenical prote	1058	99.5	3.2	392	2	B48423	homeotic protein e
986	100.5	3.2	262	2	E88400	protein H34I24.2 (	1059	99.5	3.2	393	1	VBEBD2	glycoprotein D - h
987	100.5	3.2	269	2	T26957	hypothenical prote	1060	99.5	3.2	420	2	T46910	heat-shock protein
988	100.5	3.2	274	2	T46041	hypothenical prote	1061	99.5	3.2	451	2	JC4199	probable serine/th
989	100.5	3.2	283	2	E88597	protein Y47DB.6 (	1062	99.5	3.2	476	1	C70986	probable pbpA prot
990	100.5	3.2	314	2	T48514	hypothenical prote	1063	99.5	3.2	491	2	F70699	hypothenical prote
991	100.5	3.2	384	2	T50921	carbamoyl-phosphat	1064	99.5	3.2	530	2	S22215	hypothenical prote
992	100.5	3.2	401	2	S65138	glycoprotein antig	1065	99.5	3.2	539	2	T28770	hypothenical prote
993	100.5	3.2	440	2	JC7807	Wiskott-Aldrich sy	1066	99.5	3.2	647	2	T43952	hypothenical prote
994	100.5	3.2	504	2	AG2373	hypothenical prote	1067	99.5	3.2	665	2	S62328	kinesin-like DNA b
995	100.5	3.2	504	2	S56745	mucin (clone PGW31	1068	99.5	3.2	702	2	A86383	hypothenical prote
996	100.5	3.2	512	2	E59437	F02569.2 protein (	1069	99.5	3.2	802	2	T24293	76.4K protein kina
997	100.5	3.2	597	2	JQ0107	hypothenical 66K p	1070	99.5	3.2	851	2	AD1427	hypothenical prote
998	100.5	3.2	677	2	T39713	zinc finger protei	1071	99.5	3.2	853	1	TUBONC	internalin, probab
999	100.5	3.2	798	2	T34248	hypothenical prote	1072	99.5	3.2	886	2	T35469	neural cell adhesi
1000	100.5	3.2	906	2	A43817	transforming prote	1073	99.5	3.2	903	2	T19209	probable ATP/GTP-
1001	100.5	3.2	975	2	S33121	homotetic protein C	1074	99.5	3.2	949	2	T24294	probable protein k
1002	100.5	3.2	1024	2	T27631	hypothenical prote	1075	99.5	3.2	958	2	E82994	hypothenical prote
1003	100.5	3.2	1030	1	H88859	protein ZC518.2 (I	1076	99.5	3.2	961	1	TSHUP4	glycine cleavage s
1004	100.5	3.2	1106	1	TVHUGL	transforming prote	1077	99.5	3.2	1013	2	T33470	thrombospondin 4 p
1005	100.5	3.2	1131	2	F96662	hypothenical prote	1078	99.5	3.2	1016	2	T41720	hypothenical prote
1006	100.5	3.2	1138	1	S24066	hypothenical prote	1079	99.5	3.2	1056	2	A53767	mucin MUC5B, trach
1007	100.5	3.2	1220	2	T48928	protein-tyrosine k	1080	99.5	3.2	1122	2	T47424	hypothenical prote
1008	100.5	3.2	1273	2	S58782	disease resistance	1081	99.5	3.2	1220	2	T06403	resistance complex
1009	100.5	3.2	1323	2	T30253	SECI1 protein - ye	1082	99.5	3.2	1390	2	T31353	polyprotein - Arab
1010	100.5	3.2	2327	2	T42630	spalt protein - mo	1083	99.5	3.2	1473	2	T31422	C-terminal domain-
1011	100.5	3.2	2562	2	T14266	aggreccan - bovine	1084	99.5	3.2	1742	2	T17120	cellulase (EC 3.2.
1012	100.5	3.2	3562	2	A47171	Xin protein - chic	1085	99.5	3.2	3869	2	A48205	All-1 protein +GTP
1013	100.5	3.2	4548	1	S00657	chondroitin sulfat	1086	99	3.2	3869	2	PQ0476	pistil extensin-li
1014	100	3.2	230	2	A56210	apoprotein(a) (EC	1087	99	3.2	214	2	T09854	proline-rich cell
1015	100	3.2	311	2	B62111	neu differentiatio	1088	99	3.2	307	1	GSF3	salivary glue prot
1016	100	3.2	334	2	G02409	hypothenical prote	1089	99	3.2	329	2	B41344	lutropin-choriogon
1017	100	3.2	366	2	S61796	protein kinase C-b	1090	99	3.2	329	2	D41344	lutropin-choriogon
1018	100	3.2	367	2	A33950	T-cell-specific tr	1091	99	3.2	331	2	C41344	lutropin-choriogon
1019	100	3.2	474	2	S15921	yopM protein - Yer	1092	99	3.2	358	2	T01296	leucine-rich repea
1020	100	3.2	476	2	C39481	protein IFX-VI3 -	1093	99	3.2	415	1	A34170	acrosin (EC 3.4.21
1021	100	3.2	510	2	H84824	serum response fac	1094	99	3.2	428	2	S45361	LRR47 protein - fr
1022	100	3.2	535	2	T17212	En/Spm-like transp	1095	99	3.2	447	2	T34992	probable lipoprote
1023	100	3.2	549	2	C87719	hypothenical prote	1096	99	3.2	466	2	T06416	cysteine proteinas
1024	100	3.2	556	2	D70940	protein R119.6 (Im	1097	99	3.2	511	2	AC0941	probable ABC trans
1025	100	3.2	562	2	S75308	probable PPG prote	1098	99	3.2	543	2	S25128	61K protein - Auto
1026	100	3.2	562	2	G75457	DNA ligase (EC 6.5	1099	99	3.2	564	2	I53106	gene gli protein -
1027	100	3.2	628	2	S44138	tetradicopeptide	1100	99	3.2	569	2	F75381	probable two-compo
1028	100	3.2	673	2	AF1143	polyadenylate-bind	1101	99	3.2	616	2	C75588	conserved hypotet
1029	100	3.2	698	2	T51915	internalin protein	1102	99	3.2	638	2	T51383	receptor protein k
1030	100	3.2	698	2	T17261	hypothenical prote	1103	99	3.2	641	2	C84726	probable receptor-
1031	100	3.2	699	2	T09069	probable cAMP-resp	1104	99	3.2	686	2	F96542	probable protein k
1032	100	3.2	713	2	T44447	neuregulin-3 (limp	1105	99	3.2	696	2	A41344	lutropin-choriogon
1033	100	3.2	725	2	T01268	leucine-rich repea	1106	99	3.2	701	2	S61239	hypothenical prote
1034	100	3.2	756	2	C87432	hypothenical prote	1107	99	3.2	770	1	S30293	transcription fact
1035	100	3.2	776	2	A46583	neuroendocrine-spe	1108	99	3.2	814	2	JC7389	thyroid stimulat
1036	100	3.2	881	2	T01269	serine/threonine-s	1109	99	3.2	860	2	C86203	hypothetical prote
1037	100	3.2	1109	2	C84545	probable disease r	1110	99	3.2	940	2	H86420	hypothetical prote
1038	100	3.2	1161	2	T45294	hypothetical prote	1111	99	3.2	963	2	C82630	serine proteinase
1039	100	3.2	1182	2	I48378	hairless protein -	1112	99	3.2	1000	2	C82630	hypothetical prote
1040	100	3.2	1240	2	T06404	resistance complex	1113	99	3.2	1097	2	T49187	ADP-ribosylation f
1041	100	3.2	1420	2	T37781	probable cytoskele	1114	99	3.2	1147	2	T42627	disease resistance
1042	100	3.2	1687	2	T30176	EGR repeat transme	1115	99	3.2	1217	2	T52348	apoptosis associat
1043	100	3.2	1791	2	T02345	hypothenical prote	1116	99	3.2	1317	2	T03748	hypothetical prote
1044	100	3.2	1802	2	T00020	bacterial blight-r	1117	99	3.2	1405	2	T04426	hypothetical prote
1045	100	3.2	1897	1	TDHULK	leukocyte antigen-	1118	99	3.2	1532	2	A61362	collagen alpha 1(X
1046	100	3.2	2459	2	S08315	peptide synthetase	1119	99	3.2	1538	2	E70874	probable ppsb prot
1047	99.5	3.2	108	2	T07642	cell wall protein	1120	99	3.2	1694	2	S50065	sialoadhesin - mou
1048	99.5	3.2	177	2	T07642	PEARL1 1 protein h	1121	99	3.2	1799	1	S44920	Zk688.5 protein - p
1049	99.5	3.2	230	2	A44074	Probable EGF-like	1122	99	3.2	2029	1	TDFFLK	hypothetical prote
1050	99.5	3.2	280	2	I48713	Phox2 homeodomain	1123	99	3.2	2088	2	E71436	hypothetical prote
1051	99.5	3.2	293	2	C75421	hypothetical prote	1124	99	3.2	6420	2	T30283	polyketide synthas



1125	98.5	3.1	230	2	T22763	hypothetical prote	1198	97.5	3.1	362	2	S23295	fetuin precursor -
1126	98.5	3.1	234	2	D88560	protein F58A4.1 [i	1199	97.5	3.1	429	2	JC4365	elk1 protein - mou
1127	98.5	3.1	342	2	I77461	luteinizing hormon	1200	97.5	3.1	460	2	T23087	hypothetical prote
1128	98.5	3.1	349	2	T15422	hypothetical prote	1201	97.5	3.1	464	2	S22697	extensin - Volvox
1129	98.5	3.1	379	2	S50125	larval glue protei	1202	97.5	3.1	497	2	F83634	hypothetical prote
1130	98.5	3.1	385	2	T18180	proline-rich prote	1203	97.5	3.1	511	2	T43282	alp21 protein - fi
1131	98.5	3.1	393	2	S62335	I71-7 protein - fr	1204	97.5	3.1	521	2	S54266	glycoprotein gc -
1132	98.5	3.1	434	1	A35005	u-plasminogen acti	1205	97.5	3.1	531	2	B55066	tyrosine decarboxy
1133	98.5	3.1	464	2	D72653	hypothetical prote	1206	97.5	3.1	563	2	A75594	ferredoxin-nitrite
1134	98.5	3.1	486	2	B39481	serum response fac	1207	97.5	3.1	574	1	A48501	probable protein-1
1135	98.5	3.1	514	2	A44100	cell adhesio mole	1208	97.5	3.1	587	2	T41653	probable transcrip
1136	98.5	3.1	633	2	T47346	receptor protein k	1209	97.5	3.1	614	2	T33149	hypothetical prote
1137	98.5	3.1	700	2	I77463	luteinizing hormon	1210	97.5	3.1	626	2	B70754	probable serine/th
1138	98.5	3.1	700	2	A49744	lutropin-choriogon	1211	97.5	3.1	627	1	JC6534	protein kinase 1 (
1139	98.5	3.1	707	2	A46302	FTB-associated spl	1212	97.5	3.1	627	2	AB0535	hypothetical prote
1140	98.5	3.1	770	2	T22808	hypothetical prote	1213	97.5	3.1	631	1	A36749	transcription fact
1141	98.5	3.1	803	2	F59433	RhoGAP protein [im	1214	97.5	3.1	662	2	D40228	neurexin II-beta p
1142	98.5	3.1	837	2	A42112	mucin-like peptide	1215	97.5	3.1	676	1	EDBE23	immediate-early pr
1143	98.5	3.1	862	2	E88594	protein Y48A6B.11	1216	97.5	3.1	710	2	D96728	hypothetical prote
1144	98.5	3.1	885	2	B86257	NBS/LRR disease re	1217	97.5	3.1	754	2	AC2807	OmpA family protei
1145	98.5	3.1	921	2	D86293	F7H2.22 protein -	1218	97.5	3.1	754	2	B97586	hypothetical prote
1146	98.5	3.1	947	2	T26314	hypothetical prote	1219	97.5	3.1	814	2	G02390	disintegrin-like m
1147	98.5	3.1	1087	2	T31100	probable potassium	1220	97.5	3.1	817	2	S51342	verprolin - yeast
1148	98.5	3.1	1272	2	T30248	fragile X mental r	1221	97.5	3.1	830	2	T17672	chitinase-like pro
1149	98.5	3.1	1281	2	T00346	hypothetical prote	1222	97.5	3.1	893	2	H96651	protein T3P18.19 [
1150	98.5	3.1	1309	2	T00078	probable RNA-direc	1223	97.5	3.1	909	1	AS4809	disease resistance
1151	98.5	3.1	1396	2	A44453	translation initia	1224	97.5	3.1	921	2	AE0332	conserved hypochet
1152	98.5	3.1	1774	2	B56101	collagen alpha 1(X	1225	97.5	3.1	929	2	T52517	hypothetical prote
1153	98.5	3.1	2180	2	T29764	hypothetical prote	1226	97.5	3.1	948	2	F87693	peptidase, M16 fam
1154	98.5	3.1	2339	2	A42566	omega-conotoxin-se	1227	97.5	3.1	1006	2	G86292	hypothetical prote
1155	98	3.1	182	2	T07641	PEARL1 protein h	1228	97.5	3.1	1258	2	JC5765	inositol polyphosp
1156	98	3.1	291	2	AF0123	probable antigenic	1229	97.5	3.1	1392	2	T51947	probable transcrip
1157	98	3.1	296	2	A56943	sensory/motor neur	1230	97.5	3.1	1715	2	C40228	neurexin II-alpha
1158	98	3.1	303	2	S40973	hypothetical prote	1231	97.5	3.1	1748	1	JQ1555	genome polyprotein
1159	98	3.1	352	2	S09266	Ig alpha chain C r	1232	97	3.1	191	2	F84522	probable proline-r
1160	98	3.1	416	1	A42879	advanced glycosyla	1233	97	3.1	238	2	T23867	hypothetical prote
1161	98	3.1	442	2	S50062	cell wall glycopro	1234	97	3.1	330	2	T26419	hypothetical prote
1162	98	3.1	499	2	A12449	hypothetical prote	1235	97	3.1	330	2	T05717	probable extensin
1163	98	3.1	514	2	A56201	transcription fact	1236	97	3.1	355	2	B26883	neural cell adhesi
1164	98	3.1	534	2	S21961	proline-rich prote	1237	97	3.1	357	2	A39364	GDF-1 embryonic gr
1165	98	3.1	535	2	S65762	chitinase (EC 3.2.	1238	97	3.1	379	2	AE3003	conserved hypochet
1166	98	3.1	538	2	I68093	PRR2 delta - human	1239	97	3.1	395	2	A86166	protein F21B7.6 [i
1167	98	3.1	538	2	A70836	hypothetical prote	1240	97	3.1	397	2	T00914	leucine-rich repea
1168	98	3.1	553	1	A42499	mullerian inhibiti	1241	97	3.1	400	1	A28172	spasmolysin precur
1169	98	3.1	560	1	WFH00	mullerian inhibiti	1242	97	3.1	421	1	S11674	acrosin (EC 3.4.21
1170	98	3.1	605	2	S48940	hypothetical prote	1243	97	3.1	428	1	TVHUEK	transforming prote
1171	98	3.1	614	2	S27962	modulator recognit	1244	97	3.1	452	2	D98280	hypothetical 28.0K
1172	98	3.1	631	2	C89243	protein F28C1.3 [i	1245	97	3.1	459	2	T35317	probable serine/th
1173	98	3.1	631	2	T21471	hypothetical prote	1246	97	3.1	483	2	T02226	NBS-LRR type resis
1174	98	3.1	715	2	S76492	lipoprotein nlipD -	1247	97	3.1	500	2	D97302	hypothetical prote
1175	98	3.1	728	2	H59435	phosphoinositide-3	1248	97	3.1	530	2	G70904	hypothetical prote
1176	98	3.1	750	2	T42614	probable envelope	1249	97	3.1	601	2	D89711	protein F40E10.4 [
1177	98	3.1	788	1	Q0BEE3	HHLF1 protein - hu	1250	97	3.1	601	2	T22025	hypothetical prote
1178	98	3.1	856	2	T43631	serine/threonine k	1251	97	3.1	632	2	T02627	hypothetical prote
1179	98	3.1	889	2	C86257	resistance to Pseu	1252	97	3.1	701	1	FOFV1R	gag polyprotein -
1180	98	3.1	896	2	S36326	ciathrin assembly	1253	97	3.1	860	2	JC4566	chitinase (EC 3.2.
1181	98	3.1	1006	2	JC5526	kinase-defective E	1254	97	3.1	966	2	D96662	hypothetical prote
1182	98	3.1	1216	2	T34101	hypothetical prote	1255	97	3.1	967	2	G96637	hypothetical prote
1183	98	3.1	1372	2	T25933	hypothetical prote	1256	97	3.1	1123	2	A39962	kinase-related tra
1184	98	3.1	1522	2	H88360	protein T22F7.3 [i	1257	97	3.1	1214	2	T47438	disease resistance
1185	98	3.1	1873	2	A55645	calcium channel, v	1258	97	3.1	1265	1	A37967	neural cell adhesi
1186	98	3.1	2115	2	S38480	nonstructural prote	1259	97	3.1	1690	2	T35694	ATP dependent DNA
1187	98	3.1	3190	2	T13828	CREB-binding prote	1260	97	3.1	1734	2	A54602	microtubule-associ
1188	98	3.1	3623	2	T08618	intrinsic factor-B	1261	97	3.1	2055	2	T00093	hypothetical prote
1189	98	3.1	3635	2	T10053	laminin alpha 5 ch	1262	97	3.1	2205	1	GNVY2W	genome polyprotein
1190	98	3.1	3871	2	T22812	hypothetical prote	1263	97	3.1	3034	2	T14119	seven-pass transme
1191	98	3.1	5069	2	T17464	rifamycin polyketi	1264	96.5	3.1	346	2	S19129	proline-rich prote
1192	97.5	3.1	215	2	S55925	probable arabinoga	1265	96.5	3.1	350	2	S75341	peptidyl-prolyl ci
1193	97.5	3.1	266	1	A35037	insulin-like growt	1266	96.5	3.1	419	2	G70602	hypothetical prote
1194	97.5	3.1	268	2	S71830	transcription coac	1267	96.5	3.1	430	2	I48755	hypothetical prote
1195	97.5	3.1	277	2	A46241	interferon respons	1268	96.5	3.1	444	2	B36389	mSAPla - mouse
1196	97.5	3.1	306	2	T09067	extensin-like prot	1269	96.5	3.1	485	1	S22543	transcription fact
1197	97.5	3.1	338	1	TVMSFB	transforming prote	1270	96.5	3.1	487	2	F70765	hypothetical prote



1271	96.5	3.1	514	2	A31643	cell adhesion 80K	1344	95.5	3.0	1159	2	I38465	probable potassium
1272	96.5	3.1	528	2	B75310	conserved hypotetic	1345	95.5	3.0	1255	2	T31065	diaphanous protein
1273	96.5	3.1	574	2	B35149	ipaH protein - Shi	1346	95.5	3.0	1256	2	T03096	CDO protein - rat
1274	96.5	3.1	598	2	T42070	protein serine/thr	1347	95.5	3.0	1331	2	T49813	related to gastric
1275	96.5	3.1	635	2	F70874	probable membrane	1348	95.5	3.0	1630	2	T00390	KIAA0614 protein -
1276	96.5	3.1	637	2	A75342	hypothetical prote	1349	95.5	3.0	2761	2	T21064	hypothetical prote
1277	96.5	3.1	646	2	T34532	hypothetical prote	1350	95	3.0	175	2	I38408	neu differentiation
1278	96.5	3.1	654	2	T45017	chemotaxis histidi	1351	95	3.0	227	2	C29149	proline-rich prote
1279	96.5	3.1	669	2	T08827	hypothetical prote	1352	95	3.0	227	2	G70555	hypothetical prote
1280	96.5	3.1	669	2	E96654	hypothetical prote	1353	95	3.0	239	2	S25618	hypothetical prote
1281	96.5	3.1	796	2	E96654	hypothetical prote	1354	95	3.0	241	2	D43273	hergulin precursor
1282	96.5	3.1	825	1	EDBEXD	immediate-early pr	1355	95	3.0	273	2	C70551	hypothetical prote
1283	96.5	3.1	1021	2	A86421	Receptor-like seri	1356	95	3.0	326	2	A59232	ABA-responsive pro
1284	96.5	3.1	1209	2	T00373	hypothetical prote	1357	95	3.0	338	2	T06336	proline-rich prote
1285	96.5	3.1	1241	2	T18311	hypothetical prote	1358	95	3.0	385	1	I39498	GTP cyclohydrolase
1286	96.5	3.1	1557	2	T02859	probable serine/th	1359	95	3.0	413	2	T52617	hypothetical prote
1287	96.5	3.1	2282	2	T42717	DNA-binding protei	1360	95	3.0	477	2	S53362	mucin SAC (clone J
1288	96.5	3.1	2352	2	T30201	Notch homolog prot	1361	95	3.0	494	1	A29079	lymphocyte surface
1289	96.5	3.1	26926	1	I38344	titin, cardiac mus	1362	95	3.0	502	2	A55197	Wiskott-Aldrich sy
1290	96	3.1	214	2	T10737	extensin-like cell	1363	95	3.0	636	2	A61718	neu differentiation
1291	96	3.1	240	2	A24264	proline-rich prote	1364	95	3.0	653	2	E84682	hypothetical prote
1292	96	3.1	287	2	C75494	cell division prot	1365	95	3.0	662	2	I61722	neu differentiation
1293	96	3.1	346	2	JA0159	cysteine proteinas	1366	95	3.0	667	2	T17221	hypothetical prote
1294	96	3.1	445	2	T05987	hypothetical prote	1367	95	3.0	673	2	T48012	hypothetical prote
1295	96	3.1	451	2	D88395	protein F53A3_6 li	1368	95	3.0	705	2	A35621	spore germination
1296	96	3.1	483	2	S12741	transcription fact	1369	95	3.0	712	2	G02512	interleukin-1 rece
1297	96	3.1	537	1	F0MVGV	gag polyprotein -	1370	95	3.0	760	2	T16726	hypothetical prote
1298	96	3.1	580	2	T34381	probable mucin DKF	1371	95	3.0	776	2	C96554	unknown protein [1
1299	96	3.1	594	2	S33561	ref(2)P protein -	1372	95	3.0	796	2	T48889	serine/threonine p
1300	96	3.1	598	2	T48822	hypothetical prote	1373	95	3.0	846	2	S52418	GTP-binding regula
1301	96	3.1	635	1	WMBSW6	capsid protein - h	1374	95	3.0	891	2	G84693	probable proline-r
1302	96	3.1	883	2	A96662	neural cell adhesi	1375	95	3.0	901	2	A44825	phosphoprotein, sy
1303	96	3.1	907	2	AD2951	hypothetical prote	1376	95	3.0	903	2	S60257	meltrin alpha mo
1304	96	3.1	910	2	H98331	cell division prot	1377	95	3.0	943	2	T34847	probable transcrip
1305	96	3.1	969	2	A75634	McR8-related prote	1378	95	3.0	1024	2	S18251	collagen alpha 1(X
1306	96	3.1	1216	2	T26104	hypothetical prote	1379	95	3.0	1209	2	T13153	brahma associated
1307	96	3.1	1231	2	S30185	insulin receptor s	1380	95	3.0	1324	2	T14070	peptide synthetase
1308	96	3.1	1544	2	E59431	phosphoinositide-b	1381	95	3.0	1474	2	B85188	retrotransposon li
1309	96	3.1	1615	2	B49502	protein-tyrosine-p	1382	95	3.0	1616	2	G70668	polyketide synthas
1310	96	3.1	1737	2	T00209	MEGF8 protein - hu	1383	95	3.0	1731	2	AB3045	ice nucleation pro
1311	96	3.1	1767	2	A49502	protein-tyrosine-p	1384	95	3.0	1770	2	B98241	saframycin Mx1 syn
1312	96	3.1	1844	1	RRWPTM	genome polyprotein	1385	95	3.0	1806	1	CGH01E	collagen alpha 1(X
1313	96	3.1	2529	2	A56223	transcription fact	1386	95	3.0	2090	2	T30075	hypothetical prote
1314	96	3.1	5376	2	T42215	zonadhesin - mouse	1387	95	3.0	2148	2	A56011	transcription fact
1315	95.5	3.0	188	2	D29149	proline-rich prote	1388	95	3.0	2274	2	T30258	adenomatous polyo
1316	95.5	3.0	284	2	F95320	conserved hypotet	1389	95	3.0	3084	1	MMMSA	laminin alpha-1 ch
1317	95.5	3.0	366	1	TDMSM4	monocyte surface g	1390	95	3.0	3084	1	MMMSA	high sulfur zein p
1318	95.5	3.0	382	2	S75923	threonine synthase	1391	94.5	3.0	211	2	T03381	hypothetical prote
1319	95.5	3.0	384	2	S51796	vasodilator-stimul	1392	94.5	3.0	255	2	B75309	hypothetical prote
1320	95.5	3.0	435	2	T46443	hypothetical prote	1393	94.5	3.0	255	2	S31096	proline-rich prote
1321	95.5	3.0	451	2	S71754	cellular hepatitis	1394	94.5	3.0	270	2	I38857	hypothetical prote
1322	95.5	3.0	479	2	D70676	probable PE protei	1395	94.5	3.0	277	2	I38857	microtubule-associ
1323	95.5	3.0	486	2	AB2975	succinate semialde	1396	94.5	3.0	298	2	H87533	peptidase, M23/M37
1324	95.5	3.0	486	2	A98308	artK protein (U594	1397	94.5	3.0	301	2	D87684	transcription regu
1325	95.5	3.0	501	2	S76563	hypothetical prote	1398	94.5	3.0	358	2	A61188	probable transcrip
1326	95.5	3.0	507	1	A46713	erythropoietin rec	1399	94.5	3.0	376	2	H82388	hypothetical prote
1327	95.5	3.0	553	2	C75318	hypothetical prote	1400	94.5	3.0	393	2	E82283	conserved hypotet
1328	95.5	3.0	570	2	A48636	fibropellin C prec	1401	94.5	3.0	464	2	AB3557	probable amidase P
1329	95.5	3.0	571	2	T43456	hypothetical prote	1402	94.5	3.0	569	2	T19128	hypothetical prote
1330	95.5	3.0	573	2	B70726	probable secD - My	1403	94.5	3.0	630	2	A39344	tumor-associated m
1331	95.5	3.0	624	2	T49366	myocyte-specific e	1404	94.5	3.0	665	2	B75461	probable cell wall
1332	95.5	3.0	630	2	T31798	hypothetical prote	1405	94.5	3.0	708	2	T33170	gelatinase B (EC 3
1333	95.5	3.0	650	2	S44806	F10E9.6 protein -	1406	94.5	3.0	719	2	T33170	hypothetical prote
1334	95.5	3.0	685	2	C56591	E75 B steroid rece	1407	94.5	3.0	860	2	I48839	tenascin-X - mouse
1335	95.5	3.0	710	1	S70965	serine/threonine-s	1408	94.5	3.0	921	2	S42617	collagen alpha 1(I
1336	95.5	3.0	722	2	T22355	hypothetical prote	1409	94.5	3.0	985	2	T06049	hypothetical prote
1337	95.5	3.0	749	2	E87559	hypothetical prote	1410	94.5	3.0	1006	2	T00050	hypothetical prote
1338	95.5	3.0	780	1	TVHUT	nerve growth facto	1411	94.5	3.0	1092	1	UN0635	neural cell adhesi
1339	95.5	3.0	880	2	D89756	protein T23E7.2b [	1412	94.5	3.0	1131	2	T13850	gene u-shaped prot
1340	95.5	3.0	943	2	E84429	probable receptor-	1413	94.5	3.0	1487	1	EDBEE1	immediate-early pr
1341	95.5	3.0	987	2	A54092	protein-tyrosine k	1414	94.5	3.0	1690	1	CGH01B	collagen alpha 4(I
1342	95.5	3.0	1027	2	I38759	zinc finger/leucin	1415	94.5	3.0	2062	2	G96602	probable receptor
1343	95.5	3.0	1054	2	A30239	hydroxymethylgluta	1416	94.5	3.0	2302	2	T14328	protein-tyrosine-p

probable potassium  
diaphanous protein  
CDO protein - rat  
related to gastric  
KIAA0614 protein -  
hypothetical prote  
neu differentiation  
proline-rich prote  
hypothetical prote  
hypothetical prote  
hergulin precursor  
hypothetical prote  
ABA-responsive pro  
proline-rich prote  
GTP cyclohydrolase  
hypothetical prote  
mucin SAC (clone J  
lymphocyte surface  
Wiskott-Aldrich sy  
neu differentiation  
hypothetical prote  
neu differentiation  
hypothetical prote  
hypothetical prote  
spore germination  
interleukin-1 rece  
hypothetical prote  
unknown protein [1  
serine/threonine p  
GTP-binding regula  
probable proline-r  
phosphoprotein, sy  
meltrin alpha mo  
probable transcrip  
collagen alpha 1(X  
brahma associated  
peptide synthetase  
retrotransposon li  
polyketide synthas  
ice nucleation pro  
hypothetical prote  
saframycin Mx1 syn  
collagen alpha 1(X  
hypothetical prote  
transcription fact  
adenomatous polyo  
laminin alpha-1 ch  
high sulfur zein p  
hypothetical prote  
proline-rich prote  
hypothetical prote  
microtubule-associ  
peptidase, M23/M37  
transcription regu  
probable transcrip  
hypothetical prote  
conserved hypotet  
probable amidase P  
hypothetical prote  
tumor-associated m  
probable cell wall  
gelatinase B (EC 3  
hypothetical prote  
tenascin-X - mouse  
collagen alpha 1(I  
hypothetical prote  
hypothetical prote  
neural cell adhesi  
gene u-shaped prot  
immediate-early pr  
collagen alpha 4(I  
probable receptor  
protein-tyrosine-p







A;Cross-references: UNIPROT:P35858; UNIPARC:UPI000000088A; GB:M86826; NID:g184807; PIDN:  
A;Experimental source: liver  
A;Note: sequence extracted from NCBI backbone (NCBIP:110171)  
F:75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:199-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>  
F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>  
F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>  
F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>  
F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>  
F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>  
F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>  
F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>  
F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>  
  
Query Match 9.6%; Score 302; DB 2; Length 605;  
Best Local Similarity 35.5%; Pred. No. 2.9e-10;  
Matches 98; Conservative 40; Mismatches 98; Indels 40; Gaps 11;  
  
QY 7 LLLPLLLL--LALG-----PGVOG-----CPSGCCSCQPQ-----TVCTARQGT 45  
Db 8 LALALLLSWALGPRSLGADPGTGEAGPACPAACVCSYDDDADELSVFCSSRNLTR 67  
QY 46 VPRDVPDVTGLVYVFENGITMLDASSFAGLGLQLLDLSQNOIASLRLLPRLLL----- 98  
Db 68 LPDGPVGGTQALWLDGNNSSVPPAQNLSGLFNLQGGQLSLE-PQALLGLENLCH 126  
QY 99 LDLSHNSLLALEPILDTANVEALRLAGLG---LQOLDEGLFSRLNRLHDLVDSDNQLER 155  
Db 127 LHLERNQLRSALGTF--AHTPALASUGLSNNRSLRLSDLEGLFGLSLWDLNMGWSLAV 184  
QY 156 VP-PVIRGLRGLTRLRAGNTRIAQLRPEDLAGLAALQELDVNSLSLQALPGDLSGLFPR 214  
Db 185 LPDAAPRGLSLRELVLAGN-RLAYLQPALFSGLAELRELDLSRNALRAIKANFVOLPR 243  
QY 215 LRLLAARNPFNCVCLSNFEG----PWVRESHVTLA 246  
Db 244 LQKLYLDRNLIAAVAPGAFGLGLKALRWLDLSHRVA 279  
  
RESULT 3  
NBHU1A  
platelet glycoprotein Ib alpha chain precursor - human  
N;Alternate names: membrane glycoprotein Ib alpha chain  
N;Contains: glycosialicin  
C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004  
C;Accession: A94174; A60435; A94173; S16945; I55355; A27075; A27102  
R;Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopoulou, T.; Roth, G.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5615-5619, 1987  
A;Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transmembrane p  
A;Reference number: A94174; MUID:87289655; PMID:3303030  
A;Accession: A94174  
A;Molecule type: mRNA  
A;Residues: 1-626 <LQ>  
A;Cross-references: UNIPROT:P07359; UNIPARC:UPI0000012B962; GB:J02940; NID:g183499; PIDN:  
R;Wicki, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemetson, K.J.  
Thromb. Haemost. 61, 448-453, 1989  
A;Title: Isolation and characterization of human blood platelet mRNA and construction of  
a cloning of a GPIb coding cDNA insert.  
A;Reference number: A60435; MUID:90020160; PMID:2799758  
A;Accession: A60435  
A;Molecule type: mRNA  
A;Residues: 207-467 <WIC>  
A;Cross-references: UNIPARC:UPI00000174311

R;Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5610-5614, 1987  
A;Title: Amino acid sequence of the von Willebrand factor-binding domain of platelet mem  
A;Reference number: A94173; MUID:87289654; PMID:3497398  
A;Accession: A94173  
A;Molecule type: protein  
A;Residues: 17-315 <TIT>  
A;Cross-references: UNIPARC:UPI00000174312  
R;Hess, D.; Schaller, J.; Rickli, E.E.; Clemetson, K.J.  
Eur. J. Biochem. 199, 389-393, 1991  
A;Title: Identification of the disulphide bonds in human platelet glycosialicin.  
A;Reference number: S16945; MUID:91301149; PMID:2070794  
A;Accession: S16945  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 224-237;262-270;277-282 <HES>  
A;Cross-references: UNIPARC:UPI00000174313; UNIPARC:UPI00000174314; UNIPARC:UPI00000174315  
R;Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.  
J. Biol. Chem. 267, 10055-10061, 1992  
A;Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of t  
ations.  
A;Reference number: I55355; MUID:92250564; PMID:1577776  
A;Accession: I55355  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 412-427 <RES>  
A;Cross-references: UNIPARC:UPI0000073621; GB:S34436; NID:g249176; PIDN:AAB22152.1; PID:  
A;Note: variant D  
C;Comment: Glycoprotein Ib (GPIb), a surface membrane protein of platelets, participates  
C;Comment: Platelet activation apparently involves disruption of the macromolecular compl  
C;Comment: Binding sites for von Willebrand factor and thrombin (the latter site with un  
C;Comment: Glycosialicin, which is approximately coextensive with the extracellular part  
C;Genetics:  
A;Gene: GDB:GP1BA; GPIB  
A;Cross-references: GDB:118806; OMIM:231200  
A;Map position: 17pter-17p12  
C;Complex: heterodimer with platelet glycoprotein Ib beta chain (NBHU1B)  
C;Superfamily: platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein r  
C;Keywords: blood coagulation; duplication; glycoprotein; platelet membrane; tandem repe  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:17-626/Product: platelet glycoprotein Ib alpha chain #status predicted <MPT>  
F:48-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F:72-93/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F:94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F:117-140/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F:141-164/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F:165-188/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F:189-212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F:379-430/Region: proline/threonine-rich 9-residue repeats  
F:502-540/Domain: transmembrane #status predicted <TRM>  
F:541-626/Domain: intracellular #status predicted <INT>  
F:37,175/Binding site: carboxydrate (Asn) (covalent) #status experimental  
F:308/Binding site: carboxydrate (Thr) (covalent) #status experimental  
  
Query Match 9.0%; Score 282; DB 1; Length 626;  
Best Local Similarity 24.0%; Pred. No. 4.4e-09;  
Matches 160; Conservative 72; Mismatches 244; Indels 190; Gaps 26;  
  
QY 9 LPILLLLALGPGVQCSPGSCQCSQPOT---VFCTARQGTTPRDPDTPVGLYVFEN--- 62  
Db 1 MPULLLLLLPSLPHPHPTCEVSKVASHLEVNCNKNLTALPDLPKDTTILHLENLLY 60  
QY 63 -----GITMLDASSF-----AGLPGQLLDLSQNOIASL-----RLPRLLL 98  
Db 61 TFSLATLMPYTRLTQNLNDRCELTKLVGDTLPVLGTLDSLHNLQSLPLGLQTLPALTV 120  
QY 99 LDLSHNSLLALEPIL-DTANVEALRLAGLQLOQDGLFSRLNRLHDLVDSDNQLERVP 157  
Db 121 LDVSNRRLTSLPLGALRGLGELQELYLKGNELKTLPPCLLTPTPKLKLSLANNLTLP 180  
QY 158 P-VIRGLRGLTRLRAGNTRIAQLRPEDLAGLAALQELDVNSLSLQALPGDLSG--LPPR 214  
Db 181 AGLNGLENLDTLLQEN-----SLYTIPKFFGSHLLPF 215



QY 215 LRLLAARNPNCVCLSWFGWRES-----HVTLASPEETRC----- 253  
 Db 216 AFLHG---NPWLCNCEILYFRRWLQDIAENAVYVMKQGVDFKAMTSNVASVQCDNSDKFPV 272  
 QY 254 -HFPKKNAGRLLE--LDVADFGCPATTTATVPTTRPVVREP-----TA 295  
 Db 273 KYFPGKCTGLDGEQTDLYDYPEDETDGDKVRATRTVVKPTKAHTPWGLFYGWSA 332  
 QY 296 LSSSLAPTWSPTAPATE-----APSPSTAPPTVGPV---PQ 330  
 Db 333 SLDSQMPSSLHPTQESTKEQTTPFRPWTFNFTLHMSITFTSKTPKSTTEPTSPSTSEPV 392  
 QY 331 PQDCPPSTCLNGTCHLGRHHLACLCPGFTGLYCESQMGQTRSPPTVTPRPPRSLT 390  
 Db 393 PEPAPNMTTLEPTP-----SPTTPE-----PTSEPAPSTTPEPTPIPT 431  
 QY 391 LGIEP---VSPTSRLVQLRYLOGSS--VOLRSRLTYRNLSPGDKRLVTLR--LPASLA 443  
 Db 432 IATSPILVSAATSLITPKSTFTLTTPKVSLLSTKTIPELDQPPKRLGVQLGHLESSRN 491  
 QY 444 EYTVTQLRPNATYSVCVMPLG-----PGRV-PEGSEACGEAHT 480  
 Db 492 D---PFLHPD---FCLLPLGFVVLGFWLLPASVVLILLSSVGHVKPQALDSCOGAAL 545  
 QY 481 PPAVHSHNAPVTOAREGNLP---LLI-----APALAAVLLAALAAVGAAYCVRRGRAMAA 533  
 Db 546 ITATQTTHLELQROGVTVPRAWLLFLRGLSLPTFRSSFLWVRPNRGNVGLVAGRRPSAL 605  
 QY 534 AODKGO 539  
 Db 606 SOGRGO 611

RESULT 4  
 JC1282  
 insulin-like growth factor-binding protein acid labile chain precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C:Accession: JC1282  
 R:Dai, J.; Baxter, R.C.  
 Biochem. Biophys. Res. Commun. 188, 304-309, 1992  
 A:Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth factor  
 A:Reference number: JC1282; MUID:93038676; PMID:1384485  
 A:Molecule type: mRNA  
 A:Residues: 1-603 <DAI>  
 A:Cross-references: UNIPROT:P35859; UNIPARC:UPI0000125918; GB:S46785; NID:G258002; PIDN:  
 A:Experimental source: liver  
 A>Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205  
 F:1-27/Domain: signal sequence #status predicted <SIG>  
 F:28-603/Product: insulin-like growth factor binding protein, acid labile chain #status  
 F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 9.0%; Score 281.5; DB 2; Length 603;  
 Best Local Similarity 32.4%; Pred. No. 4.5e-09;  
 Matches 92; Conservative 49; Mismatches 106; Indels 37; Gaps 11;  
 QY 6 PLLLLPLL-LALGP-GVQG-----CPSGCOCQSQPQ-----TVFCTARQGT 45  
 Db 8 PALVLLAFWALGPGCHLQGTDPGASADAEQPCVCTCSDHDDYDELSVFCSSKNLTH 67  
 QY 46 VPRDVPDVTGLYVFENGITMLDASSFAGLPGQLQLDLDSQNTIASRLPRLL-----LPRLLL 99  
 Db 68 LPDDIPVSTRALWLDGNNLSSIPSAFQNLSSLDLFLNLOGSWLRSLPEQALLGLQNLXYL 127  
 QY 100 DLSHNSLLALEPGIL-DTANVEALRLAGLQQLDEGLFSRLRNHLHDLDVSDNQLERVP- 157  
 Db 128 HLERNRLNRLVGLFTHPTPSLASLSLSSNLLGRLEEGFLGSLHLDNLGNWSLVVLPD 187  
 QY 158 PVIRGLRGLTRLAGNTRIAOLRPEDLAGLAALQELDVNSLSLOALPGDLSGLFPRLR 217  
 Db 188 TVFQGLGNLHELVLGN-KLTYLQPALFCGLGELRELDLSRNALRSVKANVFHLPRLQK 246

QY 218 LAAARNPNCVCLSWFG-----PWVRESHVTLAS-PEETRCCHPP 256  
 Db 247 LYLDNRNLITAVAPGAFGLGMKALRWLDLSHRNVAGLMEDT---FP 287  
 RESULT 5  
 JC6128  
 insulin-like growth factor binding complex acid labile chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 23-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 09-Jul-2004  
 C:Accession: JC6128  
 R:Boisclair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.  
 Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996  
 A:Title: Organization and chromosomal localization of the gene encoding the mouse acid labile  
 A:Reference number: JC6128; MUID:96413591; PMID:8816745  
 A:Accession: JC6128  
 A:Molecule type: DNA  
 A:Residues: 1-603 <BOI>  
 A:Cross-references: UNIPROT:P70389; UNIPARC:UPI0000000891; GB:U66900; NID:G1621612; PIDN:  
 C:Comment: This protein is a serum protein and it is of the ternary complex in the physical  
 C:Genetics:  
 A:Gene: als  
 A:Map position: 17

Query Match 8.9%; Score 278.5; DB 2; Length 603;  
 Best Local Similarity 32.8%; Pred. No. 6.7e-09;  
 Matches 90; Conservative 48; Mismatches 101; Indels 35; Gaps 10;  
 QY 6 PLLLLPLL-LALGP-GVQG-----CPSGCOCQSQPQ-----TVFCTARQGT 45  
 Db 8 PALVLLAFWALGPGCHLQGTDPGASADAEQPCVCTCSDHDDYDELSVFCSSRNLTQ 67  
 QY 46 VPRDVPDVTGLYVFENGITMLDASSFAGLPGQLQLDLDSQNTIASRLPRLL----- 98  
 Db 68 LPDGPVSTRALWLDGNNLSSIPSAFQNLSSLDLFLNLOGSWLRSLPEQALLGLQNLXYL 126  
 QY 99 DLSHNSLLALEPGIL-DTANVEALRLAGLQQLDEGLFSRLRNHLHDLDVSDNQLERVP 157  
 Db 127 HLERNRLNRLVGLFTHPTPSLASLSLSSNLLGRLEEGFLGSLHLDNLGNWSLVVLP 186  
 QY 158 -PVIRGLRGLTRLAGNTRIAOLRPEDLAGLAALQELDVNSLSLOALPGDLSGLFPRLR 216  
 Db 187 DTVFQGLGNLHELVLGN-KLTYLQPALFCGLGELRELDLSRNALRSVKANVFHLPRLQ 245  
 QY 217 LLAARNPNCVCLSWFG-----PWVRESHVTLA 246  
 Db 246 KLYLDNRNLITAVAPGAFGLGMKALRWLDLSHRNVA 279

RESULT 6  
 T42218  
 slit-1 protein homolog - rat  
 N:Alternate names: MEGF4 protein  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C:Accession: T42218  
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  
 Genomics 51, 27-34, 1998  
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs  
 A:Reference number: T42218; MUID:98360089; PMID:9693030  
 A:Accession: T42218  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
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 A:Cross-references: UNIPROT:O88279; UNIPARC:UPI000004F208; EMBL:AB011530; NID:G3449289; I  
 A:Experimental source: strain Sprague-Dawley; brain  
 C:Genetics:  
 A:Gene: MEGF4  
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r  
 Query Match 8.9%; Score 278; DB 2; Length 1531;  
 Best Local Similarity 25.8%; Pred. No. 2.1e-08;







C;Accession: B36665  
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.  
Genes Dev. 4, 2169-2187, 1990  
A;Title: slit: an extracellular protein necessary for development of midline glia and co  
A;Reference number: A36665; MUID:91099665; PMID:2176636  
A;Accession: B36665  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1469 <ROT>  
A;Cross-references: UNIPARC:UPI0000177454; GB:X53959  
C;Genetics:  
A;Gene: FlyBase:sl  
A;Cross-references: FlyBase:FBgn0003425  
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r  
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>  
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>  
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>  
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>  
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>  
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>  
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>  
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>  
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>  
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>  
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>  
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>  
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>  
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>  
F;1028-1061/Domain: EGF homology <EGF>  
F;1068-1099/Domain: EGF homology <EGF2>  
F;1115-1148/Domain: EGF homology <EGF1>  
Query Match 8.1%; Score 255.5; DB 2; Length 1469;  
Best Local Similarity 21.4%; Pred. No. 3.9e-07;  
Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;  
QY 24 CPSCGCSQPTVCTARQTTVPDRVP-----PDTVGLY 58  
DB 519 CPAMCHC-EGTTVDCTGRRLKEIPRDIPLHTTELLNDNDELGRISDGLFRLPHLVKLE 577  
QY 59 VFENGITMLDASSFAGLPGLQLDLSONQIAS-----LRLPRLLLDLSHNSLLALEPG 112  
DB 578 LKRNQLTGTPNFAEGASHIQELQNGENKIKETISNKFGLGHQKLTNLNDNQISCVMPG 637  
QY 113 ILDTAN-----VEALRLAGLQLODGLFSLRLNHLDLV--- 148  
DB 638 SFHLSLTLNLASPNFNCNCHLAWPAECVRKKSNGGAARCAPSKVRDQVKDLPHS 697  
QY 149 -----SDNQLERPVP---PV----- 159  
DB 698 EFKCSSENSEGGIDGVCPSCTCTGTVACSRNQLKEIPRGIPAEPTSLEYLSNEIEQI 757  
QY 160 ----IRGLGTLRLIAGNTRIAQLRPEDLAGLAALQELDVS-----NL 199  
DB 758 HYERIRHRLSLTRLDLS-NNQITLSNYTANLTKLSTLIISYNKLOCLQRHALSGLNLL 816  
QY 200 SLQALPGDLSGLFPR-----LRLAAARNPFCNCPVSWFPGWVRESHVTLASPEET 251  
DB 817 RVVSLHGNRISMLPEGSFEDLKSITHALGNSNPLYDCGCKWFSQWIKLDVY---EGIA 873  
QY 252 RCHFPNKNAGRLLELDYADFGCPATTTATVPTTRPVREPTALSSSLAPTWLSPTA 311  
DB 874 RCAEPEQMDKILSTPSSSFVCRGRVRNDILAKNCNACFEQPCQNOACV-----ALPO 927

QY 312 TEAPSPSTAPPVGVVPOP-----QDCPPSTCLNGTCHLGRHHIACLCPEG 360  
DB 928 REYQC-----LCOPGVGHKCEFMIDACYGNPCRNATCTVLEEGRFSCQCAPG 976  
QY 361 FTGLYCESOM 370  
DB 977 YTGACETNI 986  
RESULT 10  
A36665  
slit protein 1 precursor - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 30-Apr-1991 #sequence revision 30-Apr-1991 #text\_change 02-Aug-2002  
R;Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.  
A;Reference number: A36665; MUID:91099665; PMID:2176636  
A;Accession: B36665  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1480 <ROT>  
A;Cross-references: UNIPARC:UPI0000150FD1; GB:X53959; NID:G98614; PIDN:CAA37910.1; PID:G9  
R;Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.  
Cell 55, 1047-1059, 1988  
A;Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of  
A;Reference number: A31640; MUID:89077533; PMID:3144436  
A;Accession: A31640  
A;Molecule type: DNA  
A;Residues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA', 'RO2'  
A;Cross-references: UNIPARC:UPI000016BD7A; GB:M23543; NID:G340939; PID:G514357  
C;Genetics:  
A;Gene: FlyBase:sl  
A;Cross-references: FlyBase:FBgn0003425  
A;Introns: 1351/3  
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r  
C;Keyfams: alternative splicing; growth factor  
F;66-91/Domain: proteoglycan amino-terminal homology <PAH1>  
F;101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
F;125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
F;149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
F;173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
F;197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>  
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>  
F;323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
F;347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
F;371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
F;395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>  
F;419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>  
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>  
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>  
F;547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>  
F;572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>  
F;596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>  
F;620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>  
F;651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>  
F;708-733/Domain: proteoglycan amino-terminal homology <PAH4>  
F;743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>  
F;767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>  
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>  
F;1028-1061/Domain: EGF homology <EGF>  
F;1068-1099/Domain: EGF homology <EGF2>  
F;1115-1148/Domain: EGF homology <EGF1>

Query Match 8.1%; Score 255.5; DB 2; Length 1480;  
Best Local Similarity 21.4%; Pred. No. 4e-07;  
Matches 105; Conservative 52; Mismatches 168; Indels 165; Gaps 14;







QY 199 LSLQALPG-----DLGLFPRLRLAARNPFCVCLSWFGPWRES 241  
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Db 235 NSLASPEGLWASLGQPNMDRGDFISG-----NPWICDQNLSDLYRWLOAQ 282  
QY 242 HVTLASPETRCHFPKNGRLL 265  
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Db 283 KQMFQNDTRCAGPRAVKQITLL 306  
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RESULT 13  
A60164  
platelet membrane glycoprotein V precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 12-Jan-1993 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: A48030; A60164; A35483; B3483; C35483; A60432; A47507; S34329  
R;Lana, F.; Morales, M.; de La Salle, C.; Cazenave, J.P.; Clemetson, K.J.; Shimomura, T.  
J. Biol. Chem. 268, 20801-20807, 1993  
A:Title: Cloning and characterization of the gene encoding the human platelet glycoprotein V.  
A:Reference number: A48030; MUID:94012616; PMID:8407908  
A:Accession: A48030  
A:Molecule type: DNA  
A:Residues: 1-560 <LA2>  
A:Cross-references: UNIPROT:P40197; UNIPARC:UPI000004B117; EMBL:Z23091; NID:9312501; PID:R;Shimomura, T.; Fujimura, K.; Mahama, S.; Takemoto, M.; Oda, K.; Fujimoto, T.; Oyama, Blood 75, 2349-2356, 1990  
A:Title: Rapid purification and characterization of human platelet glycoprotein V: the a  
A:Reference number: A60164; MUID:90275263; PMID:2350580  
A:Accession: A60164  
A:Molecule type: protein  
A:Residues: 365-384,'X',386-390,'X',392-395,'X',397-188-208,'I',210-27-50,'X',52-53;174-  
, 'X',108,'T',61-72,'TK',75-77,'V',56-57,'G',479-487,'X',489-498,'X',500,'X',502-503,'X',  
A:Cross-references: UNIPARC:UPI000017C2F6; UNIPARC:UPI000017C2F7; UNIPARC:UPI000017C2F8;  
2FD; UNIPARC:UPI000017C2FE; UNIPARC:UPI000017C2FF; UNIPARC:UPI000017C300; UNIPARC:UPI000  
R;Roth, G.J.; Church, T.A.; McMullen, B.A.; Williams, S.A.  
Biochem. Biophys. Res. Commun. 170, 153-161, 1990  
A:Title: Human platelet glycoprotein V: a surface leucine-rich glycoprotein related to a  
A:Reference number: A35483; MUID:90321220; PMID:2372284  
A:Accession: A35483  
A:Molecule type: protein  
A:Residues: 145-166,'I',168-169,'X',171-172 <R0>  
A:Cross-references: UNIPARC:UPI000017C303  
A:Note: this proteolytic fragment was designated peptide M392  
A:Accession: B35483  
A:Molecule type: protein  
A:Residues: 121-129,'W',131-135;466-468,'X',470 <R02>  
A:Cross-references: UNIPARC:UPI000017C304; UNIPARC:UPI000017C305  
A:Note: this material was designated peptide M393 but may contain two peptides  
A:Accession: C35483  
A:Molecule type: protein  
A:Residues: 252-266,'H',268-272,'X',274-279,'I',281-284,'I',286 <R03>  
A:Cross-references: UNIPARC:UPI000017C306  
A:Note: this proteolytic fragment was designated peptide M401  
R;Zafar, R.S.; Walz, D.A. 1989  
Thromb. Res. 53, 31-44, 1989  
A:Title: Platelet membrane glycoprotein V: characterization of the thrombin-sensitive gl  
A:Reference number: A60432; MUID:89162331; PMID:2922700  
A:Accession: A60432  
A:Molecule type: protein  
A:Residues: 477-478,'FX',481-485,'E',487,'V',489-492,'NQ',495,'E',497-498 <ZAF>  
A:Cross-references: UNIPARC:UPI000017C307  
R;Hickey, M.J.; Hagen, F.S.; Vagi, M.; Roth, G.J.  
proc. Natl. Acad. Sci. U.S.A. 90, 8327-8331, 1993  
A:Title: Human platelet glycoprotein V: characterization of the polypeptide and the rela  
A:Reference number: A47507; MUID:93391348; PMID:7690959  
A:Accession: A47507  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-560 <RES>  
A:Cross-references: UNIPARC:UPI000004B117; GB:L11238; NID:9388759; PIDN:AAA03069.1; PID:  
C:Comment: This platelet membrane protein is a substrate for thrombin.  
C:Comment: The amino end of the intact protein is blocked.  
C:Comment: This protein is absent in Bernard-Soulier syndrome.  
C:Genetics:

A:Gene: GDB:GPS  
A:Cross-references: GDB:230236; OMIM:173511  
A:Map position: 5pter-5qter  
C:Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prote  
Query Match 7.7%; Score 240; DB 2; Length 560;  
Best Local Similarity 27.2%; Pred. No. 1e-06;  
Matches 109; Conservative 28; Mismatches 111; Indels 152; Gaps 14;  
QY 57 LYVFENGITMLDASSFAGLPGLQLDSQNI-----ASL--RLPRLLLDLSHNSLLALE 110  
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Db 127 LFLDHNALRGIDQNMFKLVNLQELALNQDLDFLPASLFTNLENKLLDLSGNLTHLP 186  
|||::|||  
QY 111 PGILDT-ANVEALRLAGLQQLDEGL-----FSRLNLHD 145  
|||::|||  
Db 187 KGLLGAQAQLERLLLSHNSRLVSLDLSGLNSLGAELTELOFHRNHIRSIAPCAFDRPLNLS 246  
|||::|||  
QY 146 LDVS-----DNQLERVPPVIRG----- 162  
|||::|||  
Db 247 LILSRNHAFPSALFLHSHNLTLLTLFENPLAEPLGVLFEGMGGLQELWLNRTQRTLP 306  
|||::|||  
QY 163 ---LRLRLRLAGNT---RIQLRPEDLAGLAALQELDV----- 196  
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Db 307 AAARNLRLVGLVTLSPRLSALPOGAFQGLGELQVLALHSNGLTALPDGLRLGLKLR 366  
|||::|||  
QY 197 -----SNLS-----LQALPGDLSGLFPRLRLAARNPFCV 228  
|||::|||  
Db 367 QVSLRRNLRLRALFRNLSSLESVQLDHNQLETLPQGVFGALPRLTEVLLGHNSWRCD 426  
|||::|||  
QY 229 CPLSMFGPVRSHVTLASPEE-TRCHFPKNGRLLLELDYADFQCPATTTTATVPTTR 287  
|||::|||  
Db 427 CGLGPFPLGLWRQ-HLGLVGESPPRCAGPAGAHGLPMLALPGGDABCPG-----PRGP 478  
|||::|||  
QY 288 PVVREPTLSSSLAPTWSLTAPTAPATEAPSPSTAPTVP 327  
|||::|||  
Db 479 P-PRPADSSS-----EAPVHPALAPNSSEP 503  
|||::|||  
RESULT 14  
JC7763  
neural leucine-rich repeat protein-3 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C:Accession: JC7763  
R;Fukumachi, K.; Matsuoka, Y.; Kitanaka, C.; Kuchino, Y.; Tsuda, H.  
Biochem. Biophys. Res. Commun. 287, 257-263, 2001  
A:Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the gene  
A:Reference number: JC7763; PMID:11549284  
A:Contents: Fibrosarcoma cells  
A:Accession: JC7763  
A:Molecule type: mRNA  
A:Residues: 1-707 <FUK>  
A:Cross-references: UNIPROT:Q9ESY6; UNIPARC:UPI000004F0F2; GB:AF291437  
C:Comment: This protein, a new member of the neuronal leucine-rich repeat protein family,  
in protein-protein interaction and functions as a cell adhesion molecule or soluble ligar  
C:Genetics:  
A:Gene: nlrr-3  
C:Keywords: cell adhesion  
Query Match 7.6%; Score 237; DB 2; Length 707;  
Best Local Similarity 20.7%; Pred. No. 2e-06;  
Matches 127; Conservative 80; Mismatches 222; Indels 186; Gaps 22;  
QY 6 PLLPLLLALLALGPGVQG-----CPSGCQCS-----QQTVFCTARQGTTP 47  
|||::|||  
Db 5 PLQIHVLLGLATLVAQGDKKVDCPOLCTCEIRPMWFTPRSIYWEASTVDCNDLGLNFP 64  
|||::|||  
QY 48 RDVPPTVGLYVFENGITMLDASSFAGLP-GLQLDLSQNIASL----- 91  
|||::|||  
Db 65 ARLPADTQILLQTNNIARIEHST--DFPNLTGLDLSQNLSSVTINVKMSQLLSVY 122  
|||::|||  
QY 92 -----RUPRLILLDLS-----HNSLLALEPGIL----- 114  
|||::|||



Db	123	LEENKLTPEKCLYGLSNQLQELVYVNHLLSAISPGAFVGLHNLRLHLNSRLQWINSK	182
QY	115	-----DTANVEALRL-----AGLGLOOLDEGLFSLRLNHLDDL	147
Db	183	WFEALFNLEILMLGDNPIRLIKDMNFQPLKLKLSLVIAGINLTVPPDDALVGLNLESIS	242
QY	148	VSDNQLERVP-----PVIRGLRG-----	165
Db	243	FYDNRNLNKVPOVALQKAVNLKFLDLNKNPINRIRGDFSNMLHLKELGINNPELVISDS	302
QY	166	-----LTRLRAGNTRIAQURPEDLAGLAALQELDVSNLSLQAL-PCDLSGLPRLRL	216
Db	303	LAVDNLPLDLRKIEATNPNRLSYTHPNAFFELPKLESIMLNSALSYLHGHTIESL-PNLK	361
QY	217	LAAARNPNCVPLSWFGFWVRESHVTLASPEETCHFPKPKNAGRLILLELDYADFGCPA	276
Db	362	EISHSNPIRCDVCIRWIN--MNKTNIRFMEPDSLCFVDPPEFGQGVQVHRFDM----	415
QY	277	TTTTATVPTTRPVVREPTALSSSL---APTMLSPATAPATEAPSPSTAPPTVGPVPOPD	333
Db	416	-----MEICLPLI-APESPSPILDVADSYVSLHCRATAEPQ-----PEIYWITPSGKR	463
QY	334	CPSTCLNGGTCHL-GTRHHLACLPEPGFTGLY---CESQMGQGTSPPTVTPRPPR--	387
Db	464	LEPNTLREKPYVHSEGLDIRGITPKEG--GLYTCTIATNLVAGADLKSIMIKVGGFVPODN	521
QY	388	--SLTGLIEPVSTSLVGLQRYLQSSVQLRSLRTYRNLSGPDKRLVTLRLPASLAEY	445
Db	522	NGSLNLIKIRDIRANSVLVS---WKANSKILKSSVKWTAFFVKTEDSQAAQSARIPSDVKVY	578
QY	446	TVTQLRPNATYSVCV	460
Db	579	NLTHLKPSTBYKICI	593

RESULT 15

T42626

secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)

N;Alternate names: neurogenic extracellular slit protein

C;Species: Mus musculus (house mouse)

C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C;Accession: T42626

R;Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H. Mech. Dev. 79, 57-72, 1998

A;Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in

A;Reference number: Z22177; MUID:99279238; PMID:10349621

A;Accession: T42626

A;Status: preliminary; translated from GR/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1025 <HOL>

A;Cross-references: UNIPROT:Q9R1B9; UNIPARC:UPI000000E8104; EMBL:AF074960; NID:g4151258;

C;Genetics:

C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein x

Query Match 7.48; Score 231; DB 2; Length 1025;

Best Local Similarity 24.0%; Pred. No. 6.9e-06;

Matches 89; Conservative 32; Mismatches 122; Indels 128; Gaps 13;

QY	24	CPSCGCSQQTVFCTARQGTTPRDPVDTVGLYVPENGITMTLDASSFAGLPGLQLDL	83
Db	223	CPSECTCLD-TXVRCSNKGLKVLPGKIPKDVTELYLDGNQFTLV-PKELSNYKHLTLIDL	280
QY	84	SQNOIASL-----RLPRLLLDLSHNSLLALEPGILDTANVEALRIAGLQLOLDEGLF	137
Db	281	SNNRISTLSNOXFENMTQLTLILSYNRLRCIPRPTD-----GLKSL-----	323
QY	138	SLRLNHLDLVSDNQLSERVPVIRGLRLRLAGNTRIAQLRPEDLAGLAALQELDVS	197
Db	324	-RLSLHGNDIS-----VVP-----	337
QY	198	NLSIQALFGDLSGLFPRLRLAAARNPNCVPLSWFGFWVRESHVTLASPEETRCHFPF	257

Db	338	-----EGAFNDLSA-----LSHLAIGANPLYCDNMQWLSDWKSEY---KEPGIARCAGPG	386
QY	258	KNAGRLILLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSP	317
Db	387	EWADKLLLTTPSKKFTCQ-----GPMDDITIQAKCNPCLSN	421
QY	318	PSTAPPTVGPVP-----QPQDCP-----PSTCLNGGTCHL--GTRHHLACL	356
Db	422	PCKNDGTCNNDPVDVFRCTCPYGFKGQDCDVIHACISNPKHGKGTCHLKEGENAGFWCT	481
QY	357	CPEGFTGLYCE	367
Db	482	CADGFEENCE	492

Search completed: July 27, 2006, 12:06:49

Job time : 62 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: July 27, 2006, 12:00:33 ; Search time 301 Seconds  
(without alignments)  
1837.739 Million cell updates/sec

Title: US-10-677-669-69  
Perfect score: 3135  
Sequence: 1 MCSRPVLLPLLLLLALGPG.....PLMGPPGCLQSLHAKPYI 598

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : UniProt 7.2.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3135	100.0	598	2	Q6UXL5_HUMAN	Q6uxl5 homo sapien
2	3083.5	98.4	673	2	Q6UXL4_HUMAN	Q6uxl4 homo sapien
3	3078.5	98.0	673	2	Q6EMK4_HUMAN	Q6emk4 homo sapien
4	2697.5	86.0	601	2	Q96CX1_HUMAN	Q96cx1 homo sapien
5	2491	79.5	673	2	Q8BJJ0_MOUSE	Q8bjj0 m 9 days em
6	2490	79.4	673	2	Q8RZG5_MOUSE	Q8rzs5 mus musculus
7	2484	79.2	673	2	Q9CZT5_MOUSE	Q9czt5 mus musculus
8	1213.5	38.7	661	2	Q6DF55_XENTR	Q6df55 xenopus tro
9	972.5	31.0	688	2	Q3MKM9_BRARE	Q3mkm9 brachydanio
10	927.5	29.6	643	2	Q503G2_BRARE	Q503g2 brachydanio
11	914.5	29.2	962	2	Q4S068_TETNG	Q4s068 tetraodon n
12	368.5	11.8	513	2	Q50LG9_HUMAN	Q50l99 homo sapien
13	359.5	11.5	635	1	LRFN4_HUMAN	Q6p199 homo sapien
14	351	11.2	636	1	LRFN4_MOUSE	Q80x08 mus musculus
15	351	11.2	636	2	Q3TQ68_MOUSE	Q3tq68 mus musculus
16	348	11.1	636	2	Q46G55_MOUSE	Q46g55 mus musculus
17	341	10.9	634	2	Q3UVS6_MOUSE	Q3uv56 mus musculus
18	341	10.9	660	2	Q8BLJ0_MOUSE	Q8blu0 m adult mal
19	339	10.8	521	2	Q8BHA1_MOUSE	Q8bha1 m 0 day neo
20	338	10.8	655	2	Q4SGV9_TETNG	Q4sgv9 tetraodon n
21	332	10.6	637	2	Q6A073_MOUSE	Q6a073 mus musculus
22	331.5	10.6	622	2	Q59GV4_HUMAN	Q59gv4 homo sapien
23	330	10.5	653	1	LRRC4_HUMAN	Q9hhw1 homo sapien
24	329.5	10.5	648	2	Q6DDY0_XENLA	Q6ddy0 xenopus lae
25	325.5	10.4	570	2	Q70AK2_XENLA	Q70ak2 xenopus lae
26	324	10.3	626	1	LRFN3_MOUSE	Q8bly3 mus musculus
27	324	10.3	626	2	Q505E2_MOUSE	Q505e2 mus musculus
28	323	10.3	732	2	Q4RPB8_TETNG	Q4rpb8 tetraodon n
29	322.5	10.3	682	2	Q6DJD2_XENLA	Q6ddj2 xenopus lae
30	322.5	10.3	811	2	Q7LOX0_HUMAN	Q7l0x0 homo sapien
31	322.5	10.3	887	2	Q75139_HUMAN	Q75139 homo sapien

32	322	10.3	605	1	ALS_PAPHA	002833 papio hamad
33	321	10.2	628	1	LRFN3_HUMAN	Q9bnc0 homo sapien
34	321	10.2	762	1	Q5JY13_HUMAN	Q5jy13 homo sapien
35	320.5	10.2	597	2	Q310Y3_BOVIN	Q310y3 bos taurus
36	320	10.2	660	1	FLRT2_HUMAN	Q43155 bos sapien
37	320	10.2	674	2	Q6RKD8_MOUSE	Q6rkd8 m fibronect
38	319	10.2	602	2	Q58CS0_BOVIN	Q58cs0 bos taurus
39	319	10.2	652	2	Q4SR42_RAT	Q4sr42 rattus norv
40	318.5	10.2	652	1	LRRC4_MOUSE	Q99ph1 mus musculus
41	317	10.1	778	2	Q6NU16_HUMAN	Q6nu16 homo sapien
42	312.5	10.0	648	2	Q70AK3_XENLA	Q70ak3 xenopus lae
43	312.5	10.0	935	2	Q4SBT7_TETNG	Q4sbt7 tetraodon n
44	311.5	9.9	420	1	R4RL2_MOUSE	Q7m5z0 mus musculus
45	310.5	9.9	420	1	R4RL2_RAT	Q80wd1 rattus norv
46	310.5	9.9	646	1	FLRT1_HUMAN	Q9nzu1 homo sapien
47	308	9.8	627	2	Q8NC95_HUMAN	Q8nc95 homo sapien
48	308	9.8	649	1	FLRT3_HUMAN	Q9nzu0 homo sapien
49	308	9.8	649	2	Q542Z5_HUMAN	Q542z9 homo sapien
50	307.5	9.8	626	2	Q4TBM8_TETNG	Q4tbn8 tetraodon n
51	307.5	9.8	674	2	Q8WVA2_HUMAN	Q8wva2 homo sapien
52	307	9.8	637	2	Q68F21_XENLA	Q68f21 xenopus lae
53	307	9.8	649	2	Q5R6T0_PONPY	Q5r6t0 pongo pygma
54	306.5	9.8	730	2	Q6PHP6_MOUSE	Q6php6 mus musculus
55	306.5	9.7	730	2	Q6US92_MOUSE	Q6us92 mus musculus
56	303.5	9.7	692	2	Q4GOS0_HUMAN	Q4g060 homo sapien
57	302.5	9.6	420	1	R4RL2_HUMAN	Q86un3 homo sapien
58	302.5	9.6	618	2	Q4SHD7_TETNG	Q4shd7 tetraodon n
59	302	9.6	605	1	ALS_HUMAN	P35858 homo sapien
60	302	9.6	605	2	Q8TAY0_HUMAN	Q8tay0 homo sapien
61	299.5	9.6	677	2	Q28256_CANFA	Q28256 canis famil
62	298.5	9.5	649	2	Q8SGT1_MOUSE	Q8sgt1 m 12 days e
63	298.5	9.5	663	2	Q62PQ1_MOUSE	Q62pg1 mus musculus
64	295.5	9.4	640	1	NGLI_MOUSE	Q8c031 mus musculus
65	295.5	9.4	640	2	Q505E5_MOUSE	Q505e5 mus musculus
66	294.5	9.4	647	2	Q50317_BRARE	Q50317 brachydanio
67	293.5	9.4	372	2	Q499C1_BRARE	Q499c1 brachydanio
68	293.5	9.4	809	2	Q9DBY4_MOUSE	Q9db4 m adult mal
69	292.5	9.3	640	1	NGLI_HUMAN	Q9hcj2 homo sapien
70	292.5	9.3	811	2	Q496Z2_RAT	Q496z2 rattus norv
71	292.5	9.3	837	2	Q80TV0_MOUSE	Q80tv0 mus musculus
72	288.5	9.2	372	2	Q7T2W3_BRARE	Q7t2w3 brachydanio
73	288.5	9.2	581	2	Q4SV17_TETNG	Q4sv17 tetraodon n
74	288.5	9.2	640	2	Q4JIW0_HUMAN	Q4jiw0 homo sapien
75	287.5	9.2	428	2	Q4S4W6_TETNG	Q4s4w6 tetraodon n
76	287.5	9.2	713	1	LRN5_HUMAN	Q93325 homo sapien
77	286	9.1	650	2	Q4RQ15_TETNG	Q4rq15 tetraodon n
78	285	9.1	640	2	Q4JIV9_HUMAN	Q4jiv9 homo sapien
79	284.5	9.1	457	2	Q6WZD1_BRARE	Q6wzd1 brachydanio
80	284	9.1	782	2	Q5T0V4_HUMAN	Q5t0v4 homo sapien
81	283.5	9.0	603	2	Q70211_RAT	Q70211 rattus norv
82	283	9.0	1515	2	Q9DE37_BRARE	Q9de37 brachydanio
83	282.5	9.0	745	2	Q6UXK2_HUMAN	Q6uxk2 homo sapien
84	282.5	9.0	785	2	Q9P263_HUMAN	Q9p263 homo sapien
85	282	9.0	626	1	GP1BA_HUMAN	P07359 homo sapien
86	281.5	9.0	603	1	ALS_RAT	P35859 rattus norv
87	281	9.0	738	2	Q90Z45_CHICK	Q90z45 gallus gall
88	280	8.9	633	2	Q4SR95_TETNG	Q4sr95 tetraodon n
89	279.5	8.9	331	2	Q2YDZ4_EPTST	Q2ydz4 eptatretus
90	279.5	8.9	619	2	Q570Z9_MOUSE	Q570z9 mus musculus
91	278.5	8.9	301	2	Q3KQP3_MOUSE	Q3kqp3 mus musculus
92	278.5	8.9	603	1	ALS_MOUSE	P70389 mus musculus
93	278.5	8.9	603	2	Q791Q5_MOUSE	Q791q5 mus musculus
94	278.5	8.9	687	2	Q9JIL0_MOUSE	Q9jil0 mus musculus
95	278	8.9	321	2	Q6S4K4_PETMA	Q6s4k4 petromyzon
96	278	8.9	1531	1	SLIT1_RAT	Q88279 rattus norv
97	277	8.8	330	2	Q4G1K3_EPTBU	Q4g1k3 eptatretus
98	276.5	8.8	1532	2	Q3Y6S4_BRARE	Q3y6s4 brachydanio
99	276.5	8.8	347	2	Q32QN8_EPTST	Q32qn8 eptatretus
100	276	8.8	1071	2	Q4RT16_TETNG	Q4rt16 tetraodon n
101	276	8.8	1531	1	SLIT1_MOUSE	Q80tr4 mus musculus
102	276	8.8	2623	2	Q6WR10_HUMAN	Q6wr10 homo sapien
103	275	8.8	358	2	Q2YE01_EPTST	Q2ye01 eptatretus
104	273.5	8.7	593	2	Q6UY18_HUMAN	Q6uy18 homo sapien



105	273.5	8.7	1504	1	SLIT DROME	P24014 drosophila	178	251	8.0	1021	2	Q9V430 DROME	Q9V430 drosophila
106	273	8.7	745	2	Q5RRK3 MOUSE	Q5rrk3 mus musculus	179	250	8.0	412	2	QARRU8_TETNG	QARRU8 tetraodon n
107	273	8.7	785	2	Q62PQ3 MOUSE	Q62pq3 mus musculus	180	249.5	8.0	347	2	Q32Q1_EPTST	Q32q1 eptatretus
108	272.5	8.7	1524	2	Q3S2J2 BRARE	Q3s2j2 brachydanio	181	249.5	8.0	789	1	LRFN2_HUMAN	Q9ulh4 homo sapien
109	272	8.7	372	2	Q32QO2_EPTST	Q32qo2 eptatretus	182	249.5	8.0	789	1	LRFN2_MACFA	Q9be71 macaca fasc
110	271.5	8.7	342	2	Q91XL1 MOUSE	Q91xl1 mus musculus	183	249.5	8.0	2597	2	Q6WRH9 RAT	Q6wrh9 rattus norv
111	271.5	8.7	347	2	Q32QS6 EPTST	Q32qs6 eptatretus	184	248.5	7.9	420	1	TPBG_MACFA	Q4t8y9 macaca fasc
112	271.5	8.7	1312	2	Q61PF0 CAEBR	Q61pf0 caenorhabdi	185	248	7.9	284	2	Q2YE15_EPTST	Q2ye15 eptatretus
113	271	8.6	372	2	Q32QO5 EPTST	Q32qo5 eptatretus	186	248	7.9	481	1	NYX_HUMAN	Q9gru5 homo sapien
114	271	8.6	473	1	RTN4R_HUMAN	Q9br6 homo sapien	187	248	7.9	481	2	Q2M1S4 HUMAN	Q2mls4 homo sapien
115	271	8.6	473	1	RTN4R_MACFA	Q9br6 homo sapien	188	247.5	7.9	305	2	Q4G1L3 EPTBU	Q4gl13 eptatretus
116	270.5	8.6	541	2	Q6PK41_HUMAN	Q6pk41 homo sapien	189	247.5	7.9	323	2	Q32QX2_EPTST	Q32qx2 eptatretus
117	270	8.6	478	2	Q6WZD2 BRARE	Q6wzd2 brachydanio	190	247.5	7.9	323	2	Q32QX2_EPTST	Q32qx2 eptatretus
118	270	8.6	1461	2	Q5VM18 HUMAN	Q5vm18 homo sapien	191	247.5	7.9	739	2	Q2PNW3_XENLA	Q2pnw3 xenopus lae
119	270	8.6	1534	1	SLIT1_HUMAN	Q75093 homo sapien	192	247.5	7.9	1521	1	SLIT2_MOUSE	Q9lib9 mus musculus
120	270	8.6	1534	2	Q5VM17 HUMAN	Q5vm17 homo sapien	193	247.5	7.9	1529	1	SLIT2_HUMAN	Q94813 homo sapien
121	268.5	8.6	409	2	Q5TOV2_HUMAN	Q5tov2 homo sapien	194	247.5	7.9	1530	2	Q9OWZ3_XENLA	Q9owz3 xenopus lae
122	268	8.5	417	2	Q6E4J7_PETMA	Q6e4j7 petromyzon	195	247	7.9	794	2	Q4SK16_TETNG	Q4sk16 tetraodon n
123	267.5	8.5	1512	2	Q9DE36 BRARE	Q9de36 brachydanio	196	246.5	7.9	283	2	Q2YE14_EPTST	Q2ye14 eptatretus
124	266.5	8.5	1529	2	Q7ZX12_XENLA	Q7zx12 xenopus lae	197	246.5	7.9	323	2	Q2YE02_EPTST	Q2ye02 eptatretus
125	266	8.5	460	2	Q61PL6_HUMAN	Q61pl6 homo sapien	198	246.5	7.9	371	2	Q32QP6_EPTST	Q32qp6 eptatretus
126	266	8.5	734	2	Q35930_MOUSE	Q35930 mus musculus	199	246	7.8	264	2	Q2YGV6_PETMA	Q2ygv6 petromyzon
127	265.5	8.5	1044	2	Q5ISR9_MACFA	Q5isr9 macaca fasc	200	246	7.8	306	2	Q2YE10_EPTST	Q2ye10 eptatretus
128	265	8.5	298	2	Q4G1L7_EPTBU	Q4gl17 eptatretus	201	246	7.8	308	2	Q4G1I3_EPTST	Q4gli3 eptatretus
129	265	8.5	734	2	Q5SX47_MOUSE	Q5sx47 mus musculus	202	246	7.8	346	2	Q2KIF2_BOVIN	Q2kif2 bos taurus
130	264.5	8.4	420	1	TPBG_HUMAN	Q5sk41 homo sapien	203	245.5	7.8	331	2	Q3UYU1_MOUSE	Q3uyy1 m 6 days ne
131	264	8.4	334	2	Q5VSG2_HUMAN	Q5vsg2 homo sapien	204	245.5	7.8	331	2	Q91W20_MOUSE	Q91w20 m cdna sequ
132	264	8.4	334	2	Q2IOM4_HUMAN	Q2iom4 homo sapien	205	245.5	7.8	346	2	Q32QY6_EPTBU	Q32qy6 eptatretus
133	264	8.4	352	2	Q4G1L1_EPTBU	Q4gl11 eptatretus	206	245.5	7.8	544	2	Q61X58 CAEBR	Q61x58 caenorhabdi
134	263	8.4	308	2	Q2YDZ5_EPTST	Q2ydz5 eptatretus	207	245.5	7.8	788	2	Q460M5_RAT	Q460m5 rattus norv
135	263	8.4	332	2	Q5IOE1_RAT	Q5ioe1 rattus norv	208	245	7.8	306	2	Q4G1K6_EPTST	Q4g1k6 eptatretus
136	263	8.4	1253	2	Q4TOS1_TETNG	Q4tos1 tetraodon n	209	245	7.8	321	2	Q6E4J9_PETMA	Q6e4j9 petromyzon
137	262	8.4	346	2	Q4G1L9_EPTBU	Q4gl19 eptatretus	210	245	7.8	708	1	LRN3_PONFY	Q6419 pongo pygma
138	261.5	8.3	347	1	A2GL_HUMAN	P02750 homo sapien	211	244.5	7.8	411	2	Q4S6L6_TETNG	Q4s6l6 tetraodon n
139	261	8.3	318	2	Q2YE28_EPTBU	Q2ye28 eptatretus	212	244.5	7.8	718	2	Q73675_XENLA	Q73675 xenopus lae
140	261	8.3	341	2	Q2YE06_EPTST	Q2ye06 eptatretus	213	244.5	7.8	766	1	SLIT2_RAT	Q9wvc1 rattus norv
141	261	8.3	1523	1	SLIT3_RAT	Q2ye21 eptatretus	214	244.5	7.8	788	1	LRFN2_MOUSE	Q5dl15 mus musculus
142	260	8.3	306	2	Q2YE21_EPTST	Q2ye21 eptatretus	215	244.5	7.8	1593	2	Q5DTL5_MOUSE	Q5dtl5 mus musculus
143	259	8.3	370	2	Q2YE78_EPTST	Q2ye78 eptatretus	216	244	7.8	346	2	Q32QV4_EPTST	Q32qv4 eptatretus
144	258	8.2	321	2	Q6E4D1_PETMA	Q6e4d1 petromyzon	217	244	7.8	458	2	Q6WZD3_BRARE	Q6wzd3 brachydanio
145	258	8.2	370	2	Q2YE77_EPTST	Q2ye77 eptatretus	218	244	7.8	567	1	GPV_RAT	Q98770 rattus norv
146	258	8.2	1523	1	SLIT3_HUMAN	Q2ye77 eptatretus	219	244	7.8	708	1	LRN3_HUMAN	Q9h3w5 homo sapien
147	257.5	8.2	324	2	Q4S3K9_TETNG	Q4s3k9 tetraodon n	220	243.5	7.8	347	2	Q32QO8_EPTST	Q32qo8 eptatretus
148	257.5	8.2	347	2	Q32QX0_EPTST	Q32qx0 eptatretus	221	243.5	7.8	476	1	NYX_MOUSE	P83503 mus musculus
149	257.5	8.2	501	2	Q4S2C5_TETNG	Q4szc5 tetraodon n	222	243	7.8	242	2	Q2VGV4_PETMA	Q2vgf4 petromyzon
150	257	8.2	306	2	Q2YDZ6_EPTST	Q2ydz6 eptatretus	223	243	7.8	290	2	Q2VGV3_PETMA	Q2vgv3 petromyzon
151	257	8.2	473	1	RTN4R_RAT	Q9wm75 rattus norv	224	243	7.8	321	2	Q6E4L4_PETMA	Q6e4l4 petromyzon
152	257	8.2	739	2	Q8BKM5_MOUSE	Q8bkm5 mus musculus	225	243	7.8	323	2	Q32QY0_EPTST	Q32qy0 eptatretus
153	256.5	8.2	342	2	Q4SGG5_TETNG	Q4sgg5 tetraodon n	226	242.5	7.7	355	2	Q2YE75_EPTST	Q2ye75 eptatretus
154	255.5	8.1	1095	2	Q90XG4_CHICK	Q90xg4 gallus gall	227	242.5	7.7	371	2	Q32QW7_EPTST	Q32qw7 eptatretus
155	254.5	8.1	1196	2	Q3V1M1_MOUSE	Q3v1m1 mus musculus	228	242.5	7.7	388	2	Q6ZM54_BRARE	Q6zms4 brachydanio
156	254	8.1	528	2	Q8N644_HUMAN	Q8n644 homo sapien	229	242.5	7.7	545	1	CPN2_HUMAN	P22732 homo sapien
157	254	8.1	1523	1	SLIT3_MOUSE	Q9wvb4 mus musculus	230	242.5	7.7	718	2	Q6PCK4_XENLA	Q6pck4 xenopus lae
158	254	8.1	1523	2	Q3UHN1_MOUSE	Q3uh1 mus musculus	231	242	7.7	220	2	Q2VGH4_PETMA	Q2vgh4 petromyzon
159	254	8.1	1523	2	Q5SS56_MOUSE	Q5ss56 mus musculus	232	242	7.7	266	2	Q2VGF4_PETMA	Q2vgf4 petromyzon
160	253.5	8.1	347	2	Q68CK4_HUMAN	Q68ck4 homo sapien	233	242	7.7	380	2	Q5TOV3_HUMAN	Q5tov3 homo sapien
161	253.5	8.1	429	2	Q3UPM4_MOUSE	Q3upm4 mus musculus	234	242	7.7	652	2	Q7PVZ3_ANOGA	Q7pvr3 anopheles g
162	253.5	8.1	589	2	Q6GQ06_MOUSE	Q6gq06 mus musculus	235	241.5	7.7	272	2	Q4KPI2_LAMAP	Q4kpi2 lampetra ap
163	253.5	8.1	1410	2	Q20204_CAREL	Q20204 caenorhabdi	236	241.5	7.7	311	2	Q6E4L3_PETMA	Q6e4l3 petromyzon
164	253	8.1	368	2	Q32QP3_EPTST	Q32qp3 eptatretus	237	241	7.7	330	2	Q2YDZ9_EPTST	Q2ydz9 eptatretus
165	253	8.1	426	1	TPBG_MOUSE	Q9z010 mus musculus	238	240.5	7.7	299	2	Q2YDZ3_EPTST	Q2ydz3 eptatretus
166	253	8.1	426	2	Q3UP12_MOUSE	Q3up12 mus musculus	239	240.5	7.7	333	2	Q2YB62_EPTST	Q2yb62 eptatretus
167	253	8.1	567	1	GPV_MOUSE	Q08742 mus musculus	240	240.5	7.7	333	2	Q32QX5_EPTST	Q32qx5 eptatretus
168	252.5	8.1	323	2	Q2YE08_EPTST	Q2ye08 eptatretus	241	240.5	7.7	333	2	Q32QY1_EPTST	Q32qy1 eptatretus
169	252	8.0	311	2	Q6E4L1_PETMA	Q6e4l1 petromyzon	242	240	7.7	308	2	Q2YDZ2_EPTST	Q2ydz2 eptatretus
170	252	8.0	426	1	TPBG_RAT	Q9pqr5 rattus norv	243	240	7.7	560	1	GPV_HUMAN	P40197 homo sapien
171	252	8.0	567	2	Q9QZU3_MOUSE	Q9qzu3 mus musculus	244	239.5	7.6	307	2	Q2YF04_EPTST	Q2yef04 eptatretus
172	252	8.0	567	2	Q3TA66_MOUSE	Q3ta66 mus musculus	245	239.5	7.6	370	2	Q8BGX3_MOUSE	Q8bgx3 m adult mal
173	251.5	8.0	309	2	Q2YDZ8_EPTST	Q2ydz8 eptatretus	246	239.5	7.6	786	2	Q5TU01_ANOGA	Q5tu01 anopheles g
174	251	8.0	473	1	RTN4R_MOUSE	Q99pi8 mus musculus	247	238.5	7.6	1256	2	Q7QCT2_ANOGA	Q7qct2 anopheles g
175	251	8.0	542	2	Q9N4G6_CAREL	Q9n4g6 caenorhabdi	248	238.5	7.6	347	2	Q2YF56_EPTST	Q2yfe56 eptatretus
176	251	8.0	622	2	Q7Z2Q7_HUMAN	Q7z2q7 homo sapien	249	238	7.6	323	2	Q4KPI3_9PETR	Q4kpi3 ichtthyomyzo
177	251	8.0	622	2	Q6ZW15_HUMAN	Q6zw15 homo sapien	250	238	7.6	348	2	Q2YE73_EPTST	Q2ye73 eptatretus



251	238	7.6	453	2	Q86XY1_HUMAN	Q86xy1 homo sapien	324	227	7.2	324	2	Q2YE58_EPTST	Q2ye58 eptaretus
252	238	7.6	544	2	Q8UV23_9PERC	Q8uv23 spheroioides	325	227	7.2	326	2	Q4KLL3_RAT	Q4kl13 rattus norv
253	237.5	7.6	323	2	Q2YE74_EPTST	Q2ye74 eptaretus	326	227	7.2	371	2	Q32R26_EPTBU	Q32r26 eptaretus
254	237.5	7.6	341	2	Q32R39_EPTBU	Q32r39 eptaretus	327	227	7.2	783	2	Q90XG2_CHICK	Q90xg2 gallus gall
255	237.5	7.6	391	2	Q9D3K0_MOUSE	Q9d3k0 m 6 days ne	328	227	7.2	950	2	Q90Z44_CHICK	Q90z44 gallus gall
256	237.5	7.6	1174	2	Q4S4C0_TETNG	Q4s4c0 tetraodon n	329	226.5	7.2	209	2	Q2VGN5_PETMA	Q2vgn5 petromyzon
257	237	7.6	289	2	Q4K906_LAMAP	Q4kp06 lampetra ap	330	226.5	7.2	283	2	Q4GL11_EPTST	Q4gl11 eptaretus
258	237	7.6	370	2	Q8N967_HUMAN	Q8n967 homo sapien	331	226.5	7.2	298	2	Q4KPI5_9PETR	Q4kpi5 ichtnyomyzo
259	237	7.6	578	1	LRC15_RAT	Q8r5m3 rattus norv	332	226.5	7.2	299	2	Q4GL19_EPTST	Q4gl19 eptaretus
260	237	7.6	707	1	LRRN3_RAT	Q8esy6 rattus norv	333	226.5	7.2	323	2	Q32QU1_EPTST	Q32qu1 eptaretus
261	237	7.6	1046	2	Q7P2J7_ANOGA	Q7p2j7 anophelies g	334	226.5	7.2	557	1	LG11_HUMAN	Q95970 homo sapien
262	236.5	7.5	461	2	Q4SA12_TETNG	Q4sa12 tetraodon n	335	226.5	7.2	719	1	LRFN5_HUMAN	Q96n16 homo sapien
263	236.5	7.5	715	2	Q4RY04_TETNG	Q4ry04 tetraodon n	336	226	7.2	321	2	Q4KPI6_9PETR	Q4kpi6 ichtnyomyzo
264	236	7.5	306	2	Q2YDZ7_EPTST	Q2ydz7 eptaretus	337	226	7.2	322	2	Q35QNI_EPTST	Q35qn1 eptaretus
265	236	7.5	707	1	LRRN3_MOUSE	Q8cbo6 mus musculus	338	226	7.2	364	2	Q4SQ63_TETNG	Q4sq63 tetraodon n
266	236	7.5	718	2	Q6PEZ7_XENLA	Q6pez7 xenopus lae	339	225.5	7.2	210	2	Q4SCF1_TETNG	Q4scf1 tetraodon n
267	235.5	7.5	283	2	Q2YE20_EPTST	Q2ye20 eptaretus	340	225.5	7.2	257	2	Q2VGS2_PETMA	Q2vgs2 petromyzon
268	235.5	7.5	296	2	Q4GIH6_EPTST	Q4gih6 eptaretus	341	225.5	7.2	298	2	Q6B4J3_PETMA	Q6b4j3 petromyzon
269	235.5	7.5	307	2	Q2YE00_EPTST	Q2ye00 eptaretus	342	225	7.2	733	2	Q2M032_DROPS	Q2m032 drosophila
270	235.5	7.5	307	2	Q2YE19_EPTST	Q2ye19 eptaretus	343	224.5	7.2	323	2	Q32QSO_EPTST	Q32qs0 eptaretus
271	235.5	7.5	579	1	LRC15_MOUSE	Q80x72 mus musculus	344	224.5	7.2	347	2	Q32QO0_EPTST	Q32qo0 eptaretus
272	235	7.5	574	2	Q4RRR5_TETNG	Q4rrr5 tetraodon n	345	224	7.1	218	2	Q2VGM8_PETMA	Q2vgm8 petromyzon
273	234.5	7.5	346	2	Q32R33_EPTBU	Q32r33 eptaretus	346	224	7.1	322	2	Q32QR2_EPTST	Q32qr2 eptaretus
274	234.5	7.5	488	2	Q4RK86_TETNG	Q4rk86 tetraodon n	347	223.5	7.1	209	2	Q2VGX5_PETMA	Q2vgx5 petromyzon
275	233.5	7.4	288	2	Q6EAJ4_PETMA	Q6eaj4 petromyzon	348	223.5	7.1	283	2	Q4GIH8_EPTST	Q4gih8 eptaretus
276	233.5	7.4	322	2	Q32QZ1_EPTBU	Q32qz1 eptaretus	349	223.5	7.1	323	2	Q2YE55_EPTST	Q2ye55 eptaretus
277	233.5	7.4	346	2	Q32QY9_EPTBU	Q32qy9 eptaretus	350	223.5	7.1	323	2	Q32QRO_EPTST	Q32qr0 eptaretus
278	233.5	7.4	545	2	Q5RS34_PONPY	Q5rs34 pongo pygma	351	223.5	7.1	647	2	Q4S1N0_TETNG	Q4s1n0 tetraodon n
279	233	7.4	393	2	Q32R29_EPTBU	Q32r29 eptaretus	352	223	7.1	289	2	Q6B4C8_PETMA	Q6b4c8 petromyzon
280	233	7.4	1316	2	Q9VQ25_DROME	Q9vq25 drosophila	353	223	7.1	345	2	Q2VEB3_EPTBU	Q2veb3 eptaretus
281	232.5	7.4	433	2	Q2YE85_EPTST	Q2ye85 eptaretus	354	223	7.1	349	2	Q4SH52_TETNG	Q4sh52 tetraodon n
282	232	7.4	487	2	Q4SA13_TETNG	Q4sa13 tetraodon n	355	222.5	7.1	323	2	Q2YE67_EPTST	Q2ye67 eptaretus
283	232	7.4	766	2	Q2WF71_MOUSE	Q2wf71 mus musculus	356	222.5	7.1	323	2	Q32QV2_EPTST	Q32qv2 eptaretus
284	231.5	7.4	283	2	Q4GIH4_EPTST	Q4gih4 eptaretus	357	222.5	7.1	323	2	Q32QW5_EPTST	Q32qw5 eptaretus
285	231.5	7.4	323	2	Q32OS9_EPTST	Q32os9 eptaretus	358	222.5	7.1	413	2	Q642I5_MOUSE	Q642i5 mus musculus
286	231.5	7.4	323	2	Q2YE66_EPTST	Q2ye66 eptaretus	359	222.5	7.1	557	1	LG11_RAT	Q8k4y5 rattus norv
287	231.5	7.4	588	2	Q2PPR9_MACPA	Q2ppr9 macaca fasc	360	222.5	7.1	557	2	Q5R945_PONPY	Q5r945 pongo pygma
288	231.5	7.4	840	1	SLIKE_MOUSE	Q8cl10 mus musculus	361	222.5	7.1	557	2	Q5FWS7_RAT	Q5fws7 rattus norv
289	231	7.4	294	2	Q5VT99_HUMAN	Q5vt99 homo sapien	362	222.5	7.1	792	2	Q90Z43_CHICK	Q90z43 gallus gall
290	231	7.4	324	2	Q32QP7_EPTST	Q32qp7 eptaretus	363	222	7.1	269	2	Q6E4L0_PETMA	Q6e4l0 petromyzon
291	231	7.4	347	2	Q32R08_EPTBU	Q32r08 eptaretus	364	222	7.1	348	2	Q32QN3_EPTST	Q32qn3 eptaretus
292	231	7.4	547	1	CPN2_MOUSE	Q9dbb9 mus musculus	365	222	7.1	348	2	Q32QP2_EPTST	Q32qp2 eptaretus
293	231	7.4	581	2	Q495Q6_HUMAN	Q495q6 homo sapien	366	222	7.1	348	2	Q95JJB_MACPA	Q95jjb macaca fasc
294	231	7.4	619	2	Q7QBW2_ANOGA	Q7qbw2 anophelies g	367	222	7.1	722	2	Q5PPU2_XENLA	Q5ppu2 xenopus lae
295	231	7.4	766	2	Q460M4_MOUSE	Q460m4 mus musculus	368	221.5	7.1	249	2	Q32QK2_PETMA	Q32qk2 petromyzon
296	231	7.4	787	2	Q4SW26_TETNG	Q4sw26 tetraodon n	369	221.5	7.1	323	2	Q32QW6_EPTST	Q32qw6 eptaretus
297	230.5	7.4	257	2	Q2VGP9_PETMA	Q2vgp9 petromyzon	370	221.5	7.1	323	2	Q32QV6_EPTST	Q32qv6 eptaretus
298	230.5	7.4	323	2	Q32QO3_EPTST	Q32qo3 eptaretus	371	221.5	7.1	475	2	Q4T109_TETNG	Q4t109 tetraodon n
299	230.5	7.4	687	2	Q4SCX3_TETNG	Q4scx3 tetraodon n	372	221.5	7.1	557	1	LG11_MOUSE	Q9j1a1 mus musculus
300	230	7.3	332	2	Q8QFN6_ELAQU	Q8qfn6 elaphe quad	373	221.5	7.1	719	1	LRFN5_MOUSE	Q8bxa0 mus musculus
301	230	7.3	332	2	Q8QFN7_ELAQU	Q8qfn7 elaphe quad	374	221.5	7.1	721	2	Q5DTH4_MOUSE	Q5dth4 mus musculus
302	230	7.3	872	2	Q4S2Q4_TETNG	Q4sz04 tetraodon n	375	221	7.0	286	2	Q2YE07_EPTST	Q2ye07 eptaretus
303	230	7.3	1229	2	Q4T7S0_TETNG	Q4t7s0 tetraodon n	376	221	7.0	322	2	Q32QS5_EPTST	Q32qs5 eptaretus
304	229.5	7.3	233	2	Q2VGE3_PETMA	Q2vge3 petromyzon	377	221	7.0	345	2	Q32QZ9_EPTBU	Q32qz9 eptaretus
305	229.5	7.3	323	2	Q2YB65_EPTST	Q2yb65 eptaretus	378	221	7.0	348	2	Q32QU7_EPTST	Q32qu7 eptaretus
306	229.5	7.3	323	2	Q2YE70_EPTST	Q2ye70 eptaretus	379	221	7.0	1093	1	LRIG1_HUMAN	Q96j1a1 homo sapien
307	229.5	7.3	330	2	Q32QW0_EPTST	Q32qw0 eptaretus	380	221	7.0	1528	2	Q2UZU6_AEDA	Q2uzu6 aedes aegyp
308	229.5	7.3	370	2	Q32R18_EPTBU	Q32r18 eptaretus	381	220.5	7.0	210	2	Q6E4M1_PETMA	Q6e4m1 petromyzon
309	229.5	7.3	828	2	Q8C8T7_MOUSE	Q8c8t7 mus musculus	382	220.5	7.0	306	2	Q4KP04_LAMAP	Q4kp04 lampetra ap
310	229	7.3	240	2	Q2VGN7_PETMA	Q2vgn7 petromyzon	383	220.5	7.0	322	2	Q6E4K1_PETMA	Q6e4k1 petromyzon
311	229	7.3	324	2	Q2VQT5_EPTST	Q2vqt5 eptaretus	384	220.5	7.0	323	2	Q32QN5_EPTST	Q32qn5 eptaretus
312	229	7.3	347	2	Q32R44_EPTBU	Q32r44 eptaretus	385	220.5	7.0	342	2	Q4RW94_TETNG	Q4rw94 tetraodon n
313	229	7.3	348	2	Q32QW2_EPTST	Q32qw2 eptaretus	386	220.5	7.0	515	1	LRTM2_MOUSE	Q8bga3 mus musculus
314	229	7.3	581	1	LRC15_HUMAN	Q8tf66 homo sapien	387	220.5	7.0	515	2	Q8C8L1_MOUSE	Q8c8l1 mus musculus
315	228.5	7.3	294	2	Q6E4I6_PETMA	Q6e4i6 petromyzon	388	220.5	7.0	733	2	Q24250_DROME	Q24250 drosophila
316	228.5	7.3	341	2	Q6ZSA7_HUMAN	Q6zsa7 homo sapien	389	220.5	7.0	841	1	SLIK6_HUMAN	Q9h5y7 homo sapien
317	228.5	7.3	342	2	Q4RRU5_TETNG	Q4rru5 tetraodon n	390	220	7.0	345	2	Q32R13_EPTBU	Q32r13 eptaretus
318	228	7.3	310	2	Q4RRQ4_TETNG	Q4rrq4 tetraodon n	391	220	7.0	347	2	Q32R23_EPTBU	Q32r23 eptaretus
319	228	7.3	322	2	Q32QP0_EPTST	Q32qp0 eptaretus	392	220	7.0	582	1	LRTM3_MOUSE	Q8bz81 mus musculus
320	228	7.3	838	2	Q4SP9_TETNG	Q4sp9 tetraodon n	393	220	7.0	582	2	Q3TQ03_MOUSE	Q3tqa3 m adult mal
321	227.5	7.3	356	2	Q8BXQ3_MOUSE	Q8bxq3 m adult ret	394	220	7.0	582	2	Q8BZAO_MOUSE	Q8bza0 mus musculus
322	227	7.2	311	2	Q3UY51_MOUSE	Q3uy51 m adult mal	395	220	7.0	603	2	Q4SJ27_TETNG	Q4sj27 tetraodon n
323	227	7.2	321	2	Q32R27_EPTBU	Q32r27 eptaretus	396	219.5	7.0	323	2	Q32QT4_EPTST	Q32qt4 eptaretus



397	219.5	7.0	323	2	Q32QV3_EPTST	Q32qv3 eptatretus	470	212	6.8	216	2	Q2VQU4_PETMA	Q2vqu4 petromyzon
398	219.5	7.0	323	2	Q32QW4_EPTST	Q32qw4 eptatretus	471	212	6.8	218	2	Q2VGI6_PETMA	Q2vgi6 petromyzon
399	219.5	7.0	323	2	Q32QR3_EPTST	Q32qr3 eptatretus	472	212	6.8	276	2	Q4GIJ9_EPTST	Q4gij9 eptatretus
400	219.5	7.0	593	2	Q4SNQ0_TETNG	Q4snq0 tetraodon n	473	212	6.8	324	2	Q32QM9_EPTST	Q32qm9 eptatretus
401	219	7.0	218	2	Q2VH13_PETMA	Q2vhl3 petromyzon	474	212	6.8	445	1	R4RL1_RAT	R4rl1 rat
402	219	7.0	264	2	Q2VH48_PETMA	Q2vh48 petromyzon	475	212	6.8	918	2	Q7Q3F0_ANOGA	Q7q3f0 anopheles g
403	219	7.0	334	2	Q2YB60_EPTST	Q2yb60 eptatretus	476	211.5	6.7	192	2	Q6E4I9_PETMA	Q6e4i9 petromyzon
404	219	7.0	334	2	Q6P7C4_RAT	Q6p7c4 rattus norv	477	211.5	6.7	270	2	Q6E4L7_PETMA	Q6e4l7 petromyzon
405	218.5	7.0	332	2	Q32R19_EPTBU	Q32r19 eptatretus	478	211.5	6.7	322	2	Q32R35_EPTBU	Q32r35 eptatretus
406	218.5	7.0	323	2	Q2YB76_EPTST	Q2yb76 eptatretus	479	211.5	6.7	323	2	Q32Q57_EPTST	Q32q57 eptatretus
407	218.5	7.0	359	2	Q6GTU0_HUMAN	Q6gtu0 homo sapien	480	211.5	6.7	323	2	Q2YE72_EPTST	Q2ye72 eptatretus
408	218.5	7.0	618	1	LRC21_MOUSE	Q8k099 mus musculus	481	211.5	6.7	323	2	Q32QU9_EPTST	Q32qu9 eptatretus
409	218	7.0	216	2	Q2VGN7_PETMA	Q2vgn7 petromyzon	482	211.5	6.7	518	2	Q5R7I2_PONPY	Q5r7i2 pongo pygma
410	218	7.0	264	2	Q2VGT2_PETMA	Q2vgt2 petromyzon	483	211	6.7	187	2	Q6E4I2_PETMA	Q6e4i2 petromyzon
411	218	7.0	323	2	Q32R09_EPTBU	Q32r09 eptatretus	484	211	6.7	218	2	Q2VGR7_PETMA	Q2vgr7 petromyzon
412	218	7.0	347	2	Q32R14_EPTBU	Q32r14 eptatretus	485	211	6.7	581	1	LRTM3_HUMAN	Q86vh5 homo sapien
413	217.5	6.9	288	2	Q8BR15_MOUSE	Q8br15 mus musculus	486	211	6.7	581	1	LRTM3_MACFA	Q2nkk7 homo sapien
414	217.5	6.9	615	2	Q4SL87_TETNG	Q4sl87 tetraodon n	487	211	6.7	209	2	Q2NKK7_HUMAN	Q2nkk7 petromyzon
415	217.5	6.9	695	2	Q4TLY8_TETNG	Q4tly8 tetraodon n	488	210.5	6.7	257	2	Q2VGR9_PETMA	Q2vgr9 petromyzon
416	217.5	6.9	1335	2	Q61OC7_CAEBR	Q61oc7 caenorhabdi	489	210.5	6.7	321	2	Q4GIM3_EPTBU	Q4gim3 eptatretus
417	217	6.9	322	2	Q2YB64_EPTST	Q2yb64 eptatretus	490	210.5	6.7	324	2	Q6E4L5_PETMA	Q6e4l5 petromyzon
418	217	6.9	348	2	Q32QN4_EPTST	Q32qn4 eptatretus	491	210.5	6.7	322	2	Q32R10_EPTBU	Q32r10 eptatretus
419	217	6.9	637	2	Q6DCV7_XENIA	Q6dcv7 xenopus lae	492	210.5	6.7	322	2	Q32R37_EPTBU	Q32r37 eptatretus
420	216.5	6.9	209	2	Q2VGT8_PETMA	Q2vgt8 petromyzon	493	210.5	6.7	4303	1	PKD1_HUMAN	P98i61 homo sapien
421	216	6.9	283	2	Q6E4C7_PETMA	Q6e4c7 petromyzon	494	210	6.7	264	2	Q2VGI2_PETMA	Q2vgi2 petromyzon
422	216	6.9	282	2	Q4GI16_EPTST	Q4gi16 eptatretus	495	210	6.7	324	2	Q32QS2_EPTST	Q32qs2 eptatretus
423	216	6.9	334	2	Q32QS4_EPTST	Q32qs4 eptatretus	496	210	6.7	324	2	Q32QTO_EPTST	Q32qto eptatretus
424	216	6.9	334	2	Q32QW1_EPTST	Q32qw1 eptatretus	497	210	6.7	324	2	Q32QU4_EPTST	Q32qu4 eptatretus
425	215	6.9	514	2	Q4VBX1_MOUSE	Q4vbx1 mus musculus	498	210	6.7	324	2	Q2YE50_EPTST	Q2ye50 eptatretus
426	215.5	6.9	322	2	Q32R32_EPTBU	Q32r32 eptatretus	499	210	6.7	358	1	CHAD_RAT	Q70210 rattus norv
427	215.5	6.9	323	2	Q2YB61_EPTST	Q2yb61 eptatretus	500	210	6.7	1028	2	O865R7_PIG	O865r7 sus scrofa
428	215.5	6.9	323	2	Q32Q76_EPTST	Q32q76 eptatretus	501	209.5	6.7	214	2	Q6E4H0_PETMA	Q6e4h0 petromyzon
429	215.5	6.9	329	2	Q56NG5_CIOIN	Q56ng5 ciona intes	502	209.5	6.7	322	2	Q32R06_EPTBU	Q32r06 eptatretus
430	215.5	6.9	331	1	PLIB_AGBL	Q93233 agkistrodon	503	209.5	6.7	322	2	Q32R12_EPTBU	Q32r12 eptatretus
431	215.5	6.9	612	2	Q4SVK9_TETNG	Q4svk9 tetraodon n	504	209.5	6.7	323	2	Q32QS1_EPTST	Q32qs1 eptatretus
432	215.5	6.9	737	2	Q9VU51_DROME	Q9vu51 drosophila	505	209.5	6.7	323	2	Q32QU6_EPTST	Q32qu6 eptatretus
433	215	6.9	322	2	Q32QX8_EPTST	Q32qx8 eptatretus	506	209.5	6.7	323	2	Q32QO8_EPTST	Q32qo8 eptatretus
434	215	6.9	323	2	Q32Q00_EPTST	Q32q00 eptatretus	507	209.5	6.7	533	2	Q5E9T6_BOVIN	Q5e9t6 bos taurus
435	215	6.9	323	2	Q2YB53_EPTST	Q2yb53 eptatretus	508	209	6.7	211	2	Q6E4I3_PETMA	Q6e4i3 petromyzon
436	215	6.9	323	2	Q32QV8_EPTBU	Q32qv8 eptatretus	509	209	6.7	216	2	Q2VQG6_PETMA	Q2vqg6 petromyzon
437	215	6.9	323	2	Q32R00_EPTBU	Q32r00 eptatretus	510	209	6.7	257	2	Q6E4J6_PETMA	Q6e4j6 petromyzon
438	215	6.9	324	2	Q32QO4_EPTST	Q32qo4 eptatretus	511	209	6.7	322	2	Q32QW8_EPTST	Q32qw8 eptatretus
439	215	6.9	743	2	Q6PIM7_HUMAN	Q6pim7 homo sapien	512	209	6.7	323	2	Q32R01_EPTBU	Q32r01 eptatretus
440	214.5	6.8	215	2	Q2VH33_PETMA	Q2vhl3 petromyzon	513	209	6.7	353	2	Q6UXK1_HUMAN	Q6uxk1 homo sapien
441	214.5	6.8	323	2	Q32QF5_EPTST	Q32qf5 eptatretus	514	209	6.7	358	1	CHAD_MOUSE	O55226 mus musculus
442	214.5	6.8	323	2	Q32QF4_EPTST	Q32qf4 eptatretus	515	209	6.7	358	2	Q5SUU4_MOUSE	Q5suu4 mus musculus
443	214.5	6.8	323	2	Q32QR6_EPTST	Q32qr6 eptatretus	516	209	6.7	391	2	Q4S8B7_TETNG	Q4s8b7 tetraodon n
444	214.5	6.8	329	2	Q56NG6_CIOIN	Q56ng6 ciona intes	517	209	6.7	1091	1	LRI1_MOUSE	P70193 mus musculus
445	214.5	6.8	347	2	Q32QP1_EPTST	Q32qp1 eptatretus	518	208.5	6.7	350	2	Q5RH06_BRARE	O5rh06 brachydanio
446	214.5	6.8	441	1	R4RL1_HUMAN	Q86un2 homo sapien	519	208.5	6.7	382	1	PRELP_HUMAN	P51898 homo sapien
447	214.5	6.8	716	1	LRRN1_HUMAN	Q6uxk5 homo sapien	520	208.5	6.7	382	2	Q6FHG6_HUMAN	Q6fhg6 homo sapien
448	214.5	6.8	731	2	Q4TI49_TETNG	Q4t149 tetraodon n	521	208.5	6.7	382	2	Q6FG38_HUMAN	Q6fg38 homo sapien
449	214.5	6.8	1535	2	Q23991_DROME	Q23991 drosophila	522	208.5	6.7	445	1	R4RL1_MOUSE	Q6fg38 homo sapien
450	214	6.8	295	2	Q6E4C9_PETMA	Q6e4c9 petromyzon	523	208.5	6.7	479	2	Q6X3Y5_BRARE	O6x3y5 brachydanio
451	214	6.8	323	2	Q32R42_EPTBU	Q32r42 eptatretus	524	208.5	6.7	518	1	LRTM4_HUMAN	O86vh4 homo sapien
452	214	6.8	324	2	Q2YB68_EPTST	Q2yb68 eptatretus	525	208.5	6.7	518	2	Q4F298_HUMAN	Q4fz98 homo sapien
453	214	6.8	516	1	LRTM2_HUMAN	Q43300 homo sapien	526	208.5	6.7	519	2	Q4KMX1_HUMAN	Q4kxm1 homo sapien
454	214	6.8	716	1	LRRN1_RAT	Q32q07 rattus norv	527	208.5	6.7	537	1	LGI4_HUMAN	Q8n135 homo sapien
455	214	6.8	717	2	Q4SR34_TETNG	Q4sr34 tetraodon n	528	208.5	6.7	590	2	Q6UXJ7_HUMAN	Q6uxj7 homo sapien
456	214	6.8	2828	2	Q9NR39_HUMAN	Q9nr39 homo sapien	529	208	6.6	218	2	Q2VGF5_PETMA	Q2vgf5 petromyzon
457	213.5	6.8	238	2	Q6E4U5_PETMA	Q6e4u5 petromyzon	530	208	6.6	322	2	Q2YE51_EPTST	Q2ye51 eptatretus
458	213.5	6.8	259	2	Q2YE23_EPTST	Q2ye23 eptatretus	531	208	6.6	649	2	Q9VK22_DROME	O9vk22 drosophila
459	213.5	6.8	273	2	Q4GI12_EPTBU	Q4gi12 eptatretus	532	207.5	6.6	180	2	Q6E4F0_PETMA	Q6e4f0 petromyzon
460	213.5	6.8	323	2	Q32QW9_EPTST	Q32qw9 eptatretus	533	207.5	6.6	323	2	Q32QT2_EPTST	Q32qt2 eptatretus
461	213.5	6.8	359	1	CHAD_HUMAN	O15335 homo sapien	534	207.5	6.6	330	2	Q4S074_TETNG	Q4s074 tetraodon n
462	213.5	6.8	361	1	CHAD_BOVIN	Q27972 bos taurus	535	207.5	6.6	518	2	Q6ZT31_HUMAN	Q6zt31 homo sapien
463	213	6.8	361	1	CHAD_BOVIN	Q27972 bos taurus	536	207.5	6.6	1329	1	GP124_MOUSE	O91z8 mus musculus
464	213	6.8	218	2	Q2VGT0_PETMA	Q2vgt0 petromyzon	537	207	6.6	313	1	LRC52_HUMAN	Q8n7c0 homo sapien
465	213	6.8	322	2	Q32QX1_EPTST	Q32qx1 eptatretus	538	207	6.6	323	2	Q2YB80_EPTBU	Q2yb80 eptatretus
466	213	6.8	323	2	Q32QW5_EPTST	Q32qw5 eptatretus	539	207	6.6	323	2	Q32R43_EPTBU	Q32r43 eptatretus
467	213	6.8	347	1	LRRN1_MOUSE	Q61809 mus musculus	540	207	6.6	536	2	Q6P0D2_BRARE	Q6p0d2 brachydanio
468	212.5	6.8	323	2	Q32Q53_EPTST	Q32q53 eptatretus	541	207	6.6	613	2	O50L44_CHICK	O50l44 gallus gall
469	212.5	6.8	604	2	Q4SHB8_TETNG	Q4shb8 tetraodon n	542	207	6.6	740	2	Q5JWV6_HUMAN	Q5jwv6 homo sapien



543	207	6.6	4293	2	O08852_MOUSE	O08852_mus musculus	616	202.5	6.5	829	2	Q4RIG0_TETNG	Q4RIG0_tetraodon n
544	206.5	6.6	192	2	Q2VGE9_PETMA	Q2vge9 petromyzon	617	202	6.4	271	2	Q4RP11_LAMAP	Q4rp11 lampetra ap
545	206.5	6.6	270	2	Q6E4K6_PETMA	Q6e4k6 petromyzon	618	202	6.4	300	2	Q2YE57_EPTST	Q2ye57 eptatretus
546	206.5	6.6	274	2	Q6E4B9_PETMA	Q6e4b9 petromyzon	619	202	6.4	321	2	Q32R36_EPTBU	Q32r36 eptatretus
547	206.5	6.6	274	2	Q6E4C1_PETMA	Q6e4c1 petromyzon	620	202	6.4	321	2	Q32R38_EPTBU	Q32r38 eptatretus
548	206.5	6.6	294	2	Q6E4L2_PETMA	Q6e4l2 petromyzon	621	202	6.4	324	2	Q32Q58_EPTST	Q32q58 eptatretus
549	206.5	6.6	323	2	Q32Q08_EPTST	Q32q08 eptatretus	622	202	6.4	1117	2	Q5VQM7_ORYSA	Q5vqm7 oryza sativ
550	206.5	6.6	327	2	Q5UAS7_XENLA	Q5u4s7 xenopus lae	623	202	6.4	1501	2	Q2M1B4_DROPS	Q2mb4 drosophila
551	206.5	6.6	618	2	Q9D1T0_MOUSE	Q9dt10 mus musculus	624	201.5	6.4	187	2	Q6E4D7_PETMA	Q6e4d7 petromyzon
552	206	6.6	214	2	Q2VGU6_PETMA	Q2vgu6 petromyzon	625	201.5	6.4	275	2	Q4G1J5_EPTST	Q4g1j5 eptatretus
553	206	6.6	324	2	Q32QX7_EPTST	Q32qx7 eptatretus	626	201.5	6.4	372	2	Q8CBR6_MOUSE	Q8cbr6 m adult mal
554	206	6.6	353	2	Q8WUAB_HUMAN	Q8wuab homo sapien	627	201.5	6.4	457	2	Q960D1_DROME	Q960d1 drosophila
555	206	6.6	353	2	Q9ULX9_HUMAN	Q9ulx9 homo sapien	628	201.5	6.4	524	2	Q4RG59_TETNG	Q4rg59 tetraodon n
556	206	6.6	381	1	PRELP_BOVIN	Q9gkn8 bos taurus	629	201.5	6.4	551	2	Q4RP95_TETNG	Q4rp95 tetraodon n
557	206	6.6	428	2	O14498_HUMAN	Q9gkn8 bos taurus	630	201.5	6.4	606	2	Q9BZ20_HUMAN	Q9bz20 homo sapien
558	206	6.6	539	2	Q5TPW2_ANOGA	Q5tpw2 anopheles g	631	201.5	6.4	892	2	P91644_DROME	P91644 drosophila
559	206	6.6	606	2	Q3URE9_MOUSE	Q3ure9 mus musculus	632	201.5	6.4	1527	2	Q9VZZA_DROME	Q9vzza drosophila
560	206	6.6	606	2	O8BLC0_MOUSE	O8blc0 m adult mal	633	201	6.4	213	2	Q6E4H6_PETMA	Q6e4h6 petromyzon
561	206	6.6	606	2	O8BZD4_MOUSE	O8bz4 mus musculus	634	201	6.4	218	2	Q6E4K9_PETMA	Q6e4k9 petromyzon
562	206	6.6	738	2	Q5UIA7_DROME	Q5uia7 drosophila	635	201	6.4	322	2	Q32QT1_EPTST	Q32qt1 eptatretus
563	206	6.6	1054	1	LRIIG2_MOUSE	Q52kt2 mus musculus	636	201	6.4	336	2	Q4S8M5_TETNG	Q4s8m5 tetraodon n
564	206	6.6	1127	2	Q4TAT9_TETNG	Q4tat9 tetraodon n	637	201	6.4	354	2	Q4W655_MOUSE	Q4w655 mus musculus
565	205.5	6.6	212	2	Q6E4H2_PETMA	Q6e4h2 tetraodon n	638	201	6.4	430	2	Q58F20_HUMAN	Q58f20 homo sapien
566	205.5	6.6	479	2	O6DH76_BRARE	Q6dh76 brachydanio	639	201	6.4	602	1	LRC40_HUMAN	Lrc40 homo sapien
567	205.5	6.6	492	2	Q99KT6_MOUSE	Q99kt6 mus musculus	640	201	6.4	712	2	Q5BL20_BRARE	Q5bl20 brachydanio
568	205.5	6.6	590	1	LRTW4_MOUSE	Q80x99 mus musculus	641	200.5	6.4	845	1	SLIK2_HUMAN	Slk2 homo sapien
569	205	6.5	248	2	Q4G1K4_EPTST	Q4g1k4 eptatretus	642	200.5	6.4	845	2	Q2KHN3_HUMAN	Q2khn3 homo sapien
570	205	6.5	256	2	Q4G1L6_EPTBU	Q4g1l6 eptatretus	643	200.5	6.4	1336	2	Q2XXV6_DROYA	Q2xxv6 drosophila
571	205	6.5	320	2	Q32QR9_EPTST	Q32qr9 eptatretus	644	200.5	6.4	1337	2	Q2XXV7_DROYA	Q2xxv7 drosophila
572	205	6.5	322	2	Q2YE54_EPTST	Q2ye54 eptatretus	645	200	6.4	218	2	Q2XVG1_PETMA	Q2xvg1 petromyzon
573	205	6.5	322	2	Q2YE63_EPTST	Q2ye63 eptatretus	646	200	6.4	280	2	Q2YE26_EPTBU	Q2ye26 eptatretus
574	205	6.5	322	2	Q32QN6_EPTST	Q32qn6 eptatretus	647	200	6.4	460	2	Q4RK03_TETNG	Q4rk03 tetraodon n
575	205	6.5	324	2	Q2YEB4_EPTST	Q2yeb4 eptatretus	648	200	6.4	616	2	Q58A95_CABEL	Q58a95 caenorhabdi
576	205	6.5	486	2	Q4RU74_TETNG	Q4ru74 tetraodon n	649	200	6.4	653	2	Q02329_CABEL	Q02329 caenorhabdi
577	205	6.5	614	2	O5RDJ4_PONPY	O5rdj4 pongo pygma	650	199.5	6.4	227	2	Q4SP28_TETNG	Q4sp28 tetraodon n
578	205	6.5	614	2	O9N008_MACFA	O9n008 macaca fasc	651	199.5	6.4	261	2	Q4G1L4_EPTBU	Q4g1l4 eptatretus
579	205	6.5	620	2	Q96PE5_HUMAN	Q96fe5 homo sapien	652	199.5	6.4	319	2	Q32QN9_EPTST	Q32qn9 eptatretus
580	205	6.5	740	1	CT075_HUMAN	Q8wu4 homo sapien	653	199.5	6.4	622	2	Q66HV9_BRARE	Q66hv9 brachydanio
581	204.5	6.5	322	2	Q32R03_EPTBU	Q32r03 eptatretus	654	199	6.3	260	2	Q2YE05_EPTST	Q2ye05 eptatretus
582	204.5	6.5	323	2	Q32QV2_EPTST	Q32qv2 eptatretus	655	199	6.3	298	2	Q32QW3_EPTST	Q32qw3 eptatretus
583	204.5	6.5	463	2	O8C1V9_MOUSE	O8c1v9 mus musculus	656	199	6.3	322	2	Q32QV8_EPTST	Q32qv8 eptatretus
584	204	6.5	196	2	Q2VGM9_PETMA	Q2vgm9 petromyzon	657	199	6.3	322	2	Q32QV5_EPTST	Q32qv5 eptatretus
585	204	6.5	276	2	Q2YE25_EPTST	Q2ye25 eptatretus	658	199	6.3	323	2	Q32QV5_EPTBU	Q32qv5 eptatretus
586	204	6.5	323	2	Q2YEB1_EPTBU	Q2yeb1 eptatretus	659	199	6.3	323	2	Q32R07_EPTBU	Q32r07 eptatretus
587	204	6.5	323	2	Q32R20_EPTBU	Q32r20 eptatretus	660	199	6.3	323	2	Q32R24_EPTBU	Q32r24 eptatretus
588	204	6.5	353	2	Q6QWY6_RAT	Q6qwy6 rattus norv	661	199	6.3	324	2	Q32QT9_EPTST	Q32qt9 eptatretus
589	204	6.5	1173	2	O9V7J8_DROME	O9v7j8 drosophila	662	199	6.3	846	1	SLIK2_MOUSE	Slk2 mus musculus
590	204	6.5	1306	2	Q6P4S1_XENLA	Q6p4s1 xenopus lae	663	199	6.3	862	2	Q4SST3_TETNG	Q4sst3 tetraodon n
591	203.5	6.5	219	2	Q2VGZ2_PETMA	Q2vgz2 petromyzon	664	199	6.3	1328	2	Q21043_CABEL	Q21043 caenorhabdi
592	203.5	6.5	299	2	Q32QX3_EPTST	Q32qx3 eptatretus	665	198.5	6.3	259	2	Q4G1J4_EPTST	Q4g1j4 eptatretus
593	203.5	6.5	845	2	Q6A1I3_HUMAN	Q6a1i3 homo sapien	666	198.5	6.3	320	2	Q6YN44_HUMAN	Q6yn44 homo sapien
594	203.5	6.5	894	2	O9VKG1_DROME	O9vkg1 drosophila	667	198.5	6.3	322	2	Q32R17_EPTBU	Q32r17 eptatretus
595	203.5	6.5	1061	2	Q53WE4_ORYSA	Q53we4 oryza sativ	668	198.5	6.3	617	1	LRC21_RAT	Lrc21 rattus norv
596	203.5	-6.5	1055	1	LRIIG2_HUMAN	Q94898 homo sapien	669	198.5	6.3	741	2	Q4SWG5_TETNG	Q4swg5 tetraodon n
597	203	6.5	218	2	Q2VGC8_PETMA	Q2vgc8 petromyzon	670	198.5	6.3	873	2	Q7XR24_ORYSA	Q7xr24 oryza sativ
598	203	6.5	269	2	Q6E4B6_PETMA	Q6e4b6 petromyzon	671	198.5	6.3	1331	1	GP124_HUMAN	Gp124 homo sapien
599	203	6.5	286	2	Q2YE17_EPTST	Q2ye17 eptatretus	672	198	6.3	192	2	Q2VH08_PETMA	Q2vh08 petromyzon
600	203	6.5	321	2	Q32QZ4_EPTBU	Q32qz4 eptatretus	673	198	6.3	298	2	Q32QN7_EPTST	Q32qn7 eptatretus
601	203	6.5	323	2	Q32R15_EPTBU	Q32r15 eptatretus	674	198	6.3	322	2	Q32QP4_EPTST	Q32qp4 eptatretus
602	203	6.5	344	2	Q2YER1_EPTST	Q2yer1 eptatretus	675	198	6.3	323	2	Q32R22_EPTBU	Q32r22 eptatretus
603	203	6.5	324	2	Q32QR5_EPTST	Q32qr5 eptatretus	676	198	6.3	323	2	Q32R16_EPTBU	Q32r16 eptatretus
604	203	6.5	428	2	Q5NVQ6_PONPY	Q5nvq6 pongo pygma	677	198	6.3	324	2	Q32QP8_EPTST	Q32qp8 eptatretus
605	203	6.5	602	1	LRC40_MACFA	Lrc40 macaca fasc	678	198	6.3	363	2	Q7SYE5_BRARE	Q7sy5e5 brachydanio
606	203	6.5	703	2	Q4SLZ4_TETNG	Q4slz4 tetraodon n	679	198	6.3	602	1	LRC40_PONPY	Lrc40 pongo pygma
607	203	6.5	1514	2	Q6NNA9_DROME	Q6nna9 drosophila	680	197.5	6.3	193	2	Q2VGP6_PETMA	Q2vgp6 petromyzon
608	203	6.5	1514	2	Q9NBK9_DROME	Q9nbk9 drosophila	681	197.5	6.3	280	2	Q6E4K3_PETMA	Q6e4k3 petromyzon
609	203	6.5	1514	2	Q9VUN0_DROME	Q9vun0 drosophila	682	197.5	6.3	300	2	Q6E4K8_PETMA	Q6e4k8 petromyzon
610	202.5	6.5	197	2	Q2VGR8_PETMA	Q2vgr8 petromyzon	683	197.5	6.3	323	2	Q32QU3_EPTST	Q32qu3 eptatretus
611	202.5	6.5	209	2	Q2VGV9_PETMA	Q2vgv9 petromyzon	684	197.5	6.3	441	2	Q4VBZ3_HUMAN	Q4vzb3 homo sapien
612	202.5	6.5	259	2	Q4G1K1_EPTST	Q4g1k1 eptatretus	685	197.5	6.3	537	2	Q9VE49_DROME	Q9ve49 drosophila
613	202.5	6.5	259	2	Q4G1H5_EPTST	Q4g1h5 eptatretus	686	197.5	6.3	548	1	LG13_HUMAN	Lg13 homo sapien
614	202.5	6.5	274	2	Q6E4J2_PETMA	Q6e4j2 petromyzon	687	197.5	6.3	548	2	Q4R4H3_MACFA	Q4r4h3 macaca fasc
615	202.5	6.5	322	2	Q32QZ8_EPTBU	Q32qz8 eptatretus	688	197.5	6.3	818	2	Q4S1X2_TETNG	Q4s1x2 tetraodon n



689	197.5	6.3	835	2	Q4SFB0_TETNG	Q4sfb0 tetraodon n	762	193	6.2	321	2	Q32R11_EPTBU	Q32r11 eptatretus
690	197.5	6.3	1321	1	GP125_HUMAN	Q8iwk6 homo sapien	763	193	6.2	324	2	Q32QN2_EPTST	Q32qn2 eptatretus
691	197	6.3	248	2	Q2YE16_EPTST	Q2ye16 eptatretus	764	193	6.2	327	2	Q4SZU8_TETNG	Q4szu8 tetraodon n
692	197	6.3	320	2	Q32Q09_EPTST	Q32qg9 eptatretus	765	193	6.2	538	2	Q2LZK6_DROPS	Q2lzk6 drosophila
693	197	6.3	332	2	Q32Q06_EPTST	Q32qg6 eptatretus	766	193	6.2	550	2	Q2VJN8_DROME	Q2vjn8 drosophila
694	197	6.3	345	2	Q9HBL6_HUMAN	Q9hbl6 homo sapien	767	192.5	6.1	185	2	Q2VGZ4_PETMA	Q2vgz4 petromyzon
695	197	6.3	694	2	Q6VYX5_ORYZA	Q6vyx5 oryza sativ	768	192.5	6.1	187	2	Q6E4D5_PETMA	Q6e4d5 petromyzon
696	197	6.3	1093	2	Q6VYX5_ORYZA	Q6vyx5 oryza sativ	769	192.5	6.1	195	2	Q2VH18_PETMA	Q2vh18 petromyzon
697	196.5	6.3	209	2	Q5XWD3_HUMAN	Q5xwd3 homo sapien	770	192.5	6.1	214	2	Q6E4G0_PETMA	Q6e4g0 petromyzon
698	196.5	6.3	259	2	Q2VGH6_PETMA	Q2vgh6 petromyzon	771	192.5	6.1	259	2	Q4G1H7_EPTST	Q4g1h7 eptatretus
699	196.5	6.3	259	2	Q2VGH6_PETMA	Q2vgh6 petromyzon	772	192.5	6.1	270	2	Q6E4K0_PETMA	Q6e4k0 petromyzon
700	196.5	6.3	261	2	Q4G1J3_EPTST	Q4g1j3 eptatretus	773	192.5	6.1	299	2	Q32QV1_EPTST	Q32qv1 eptatretus
701	196.5	6.3	322	2	Q4G1J1_EPTST	Q4g1j1 eptatretus	774	192.5	6.1	322	2	Q32QV3_EPTBU	Q32qv3 eptatretus
702	196.5	6.3	322	2	Q32QY4_EPTBU	Q32qy4 eptatretus	775	192.5	6.1	428	2	Q6GU68_MOUSE	Q6gu68 mus musculus
703	196.5	6.3	332	2	Q2L292_DROPS	Q2l292 drosophila	776	192.5	6.1	542	2	Q5OD27_MOUSE	Q5od27 mus musculus
704	196.5	6.3	1332	2	Q2XXW5_DROBE	Q2xxw5 drosophila	777	192.5	6.1	575	2	Q33580_CABEL	Q33580 caenorhabdi
705	196	6.3	1333	2	Q2XXW0_DROME	Q2xxw0 drosophila	778	192.5	6.1	887	2	Q2XI21_DROBE	Q2xi21 drosophila
706	196	6.3	263	2	Q6E4D0_PETMA	Q6e4d0 petromyzon	779	192.5	6.1	1093	2	Q6HA06_CRAGI	Q6ha06 crassostrea
707	196	6.3	300	2	Q32QX6_EPTST	Q32qx6 eptatretus	780	192	6.1	265	2	Q6E4K2_PETMA	Q6e4k2 petromyzon
708	195.5	6.2	3638	2	Q15142_HUMAN	Q15142 homo sapien	781	192	6.1	273	2	Q6E4K5_PETMA	Q6e4k5 petromyzon
709	195.5	6.2	298	2	Q32QZ6_EPTBU	Q32qz6 eptatretus	782	192	6.1	300	2	Q2VE86_EPTST	Q2ve86 eptatretus
710	195.5	6.2	323	2	Q2YE59_EPTST	Q2ye59 eptatretus	783	192	6.1	548	1	LG13_MOUSE	Q8k406 mus musculus
711	195.5	6.2	370	2	Q5BD17_BOVIN	Q5bd17 bos taurus	784	192	6.1	548	2	Q3VIR3_MOUSE	Q3vir3 mus musculus
712	195.5	6.2	378	1	PRELP_MOUSE	Q9jk53 mus musculus	785	192	6.1	627	2	Q6UN14_LEICH	Q6un14 leishmania
713	195.5	6.2	378	2	Q543S0_MOUSE	Q543s0 mus musculus	786	191.5	6.1	185	2	Q2VGS8_PETMA	Q2vgs8 petromyzon
714	195.5	6.2	931	2	Q86PM1_DROME	Q86pm1 drosophila	787	191.5	6.1	187	2	Q6E417_PETMA	Q6e417 petromyzon
715	195	6.2	322	2	Q9VM16_DROME	Q9vm16 drosophila	788	191.5	6.1	193	2	Q2VGY8_PETMA	Q2vgy8 petromyzon
716	195	6.2	440	2	Q32QP9_EPTST	Q32qp9 eptatretus	789	191.5	6.1	204	2	Q6E4J8_PETMA	Q6e4j8 petromyzon
717	195	6.2	614	2	Q4RSH2_MACFA	Q4rsh2 macaca fasc	790	191.5	6.1	915	2	Q9ERV7_MOUSE	Q9erv7 mus musculus
718	195	6.2	620	2	Q6NUK3_HUMAN	Q6nuk3 homo sapien	791	191.5	6.1	980	1	SLIK3_MOUSE	Q8l0b9 mus musculus
719	195	6.2	620	2	Q6UXM3_HUMAN	Q6uxm3 homo sapien	792	191.5	6.1	980	2	Q6NZM5_MOUSE	Q6nmz5 mus musculus
720	195	6.2	837	1	SLIK4_HUMAN	Q8iw52 homo sapien	793	191	6.1	192	2	Q2VGN8_PETMA	Q2vgn8 petromyzon
721	194.5	6.2	837	2	Q5JXG3_HUMAN	Q5jxg3 homo sapien	794	191	6.1	194	2	Q2VGE8_PETMA	Q2vge8 petromyzon
722	194.5	6.2	322	2	Q2YEB2_EPTBU	Q2yeb2 eptatretus	795	191	6.1	271	2	Q4RP00_LAWAP	Q4k900 lampetra ap
723	194.5	6.2	323	2	Q32QV9_EPTST	Q32qv9 eptatretus	796	191	6.1	440	2	Q5SRC8_PONPY	Q5src8 pongo pygma
724	194.5	6.2	369	2	Q65291_CHICK	Q65291 gallus gall	797	191	6.1	610	2	Q4T1M0_TETNG	Q4t1m0 tetraodon n
725	194.5	6.2	680	2	Q3MH9_BOVIN	Q3mh9 bos taurus	798	191	6.1	868	2	Q2XQ10_CHICK	Q2xq10 gallus gall
726	194.5	6.2	693	2	Q7Z3D0_HUMAN	Q7z3d0 homo sapien	799	190.5	6.1	251	2	Q4G117_EPTST	Q4g117 eptatretus
727	194.5	6.2	699	1	ECM2_HUMAN	Q94769 homo sapien	800	190.5	6.1	894	2	Q5H721_FUGRU	Q5h721 fugu rubrip
728	194.5	6.2	699	2	Q5T9F2_HUMAN	Q5t9f2 homo sapien	801	190.5	6.1	1238	2	Q6NR19_DROME	Q6nr19 drosophila
729	194.5	6.2	737	2	Q965M3_CABEL	Q965m3 caenorhabdi	802	190.5	6.1	1535	2	Q9VPF0_DROME	Q9vpf0 drosophila
730	194.5	6.2	881	2	Q965M2_CABEL	Q965m2 caenorhabdi	803	190	6.1	191	2	Q6E4H3_PETMA	Q6e4h3 petromyzon
731	194	6.2	1630	1	LAP4_HUMAN	Q14160 homo sapien	804	190	6.1	639	2	Q6E4N6_CABER	Q6e4n6 tetraodon n
732	194	6.2	192	2	Q2VGJ7_PETMA	Q2vgj7 petromyzon	805	190	6.1	654	2	Q628N6_CABER	Q628n6 caenorhabdi
733	194	6.2	258	2	Q4G110_EPTST	Q4g110 eptatretus	806	190	6.1	733	1	CT075_MOUSE	P59383 mus musculus
734	194	6.2	258	2	Q4G1J0_EPTST	Q4g1j0 eptatretus	807	190	6.1	1119	1	LRIG3_HUMAN	Q6uxml homo sapien
735	194	6.2	263	2	Q6E4C0_PETMA	Q6e4c0 petromyzon	808	190	6.1	1346	2	Q9V477_DROME	Q9v477 drosophila
736	194	6.2	320	2	Q32Q73_EPTST	Q32q73 eptatretus	809	190	6.1	2800	2	Q6XHB1_DICDI	Q6xhb1 dictyosteli
737	194	6.2	611	2	Q4RHK3_TETNG	Q4rhk3 tetraodon n	810	189.5	6.0	252	2	Q4G1J7_EPTST	Q4g1j7 eptatretus
738	194	6.2	692	2	Q4RV46_TETNG	Q4rv46 tetraodon n	811	189.5	6.0	370	2	Q4RSX9_TETNG	Q4rsx9 tetraodon n
739	193.5	6.2	836	2	Q9V9V6_DROME	Q9v9v6 drosophila	812	189.5	6.0	880	2	Q2XY23_DROYA	Q2xy23 drosophila
740	193.5	6.2	186	2	Q6E4H8_PETMA	Q6e4h8 petromyzon	813	189	6.0	192	2	Q2VGJ2_PETMA	Q2vgj2 petromyzon
741	193.5	6.2	270	2	Q4KP03_LAWAP	Q4kp03 lampetra ap	814	189	6.0	298	2	Q32QU2_EPTST	Q32qu2 eptatretus
742	193.5	6.2	273	2	Q4G1M1_EPTBU	Q4g1m1 eptatretus	815	189	6.0	369	1	PGS1_MOUSE	P28653 mus musculus
743	193.5	6.2	377	1	PRELP_RAT	Q9eqp5 rattus norv	816	189	6.0	369	1	PGS1_RAT	P47853 rattus norv
744	193.5	6.2	378	2	Q8CAZ5_MOUSE	Q8caz5 mus musculus	817	189	6.0	369	2	Q3TNV9_MOUSE	Q3tnv9 m 15 days e
745	193.5	6.2	421	2	Q9NT99_HUMAN	Q9nt99 homo sapien	818	189	6.0	627	2	Q4T5R5_TETNG	Q4t5r5 tetraodon n
746	193.5	6.2	433	2	Q6IDG7_DROME	Q6idg7 drosophila	819	189	6.0	760	2	Q4QG18_LEIMA	Q4qg18 leishmania
747	193.5	6.2	545	1	LG12_HUMAN	Q9n0v4 homo sapien	820	189	6.0	839	2	Q9SN46_ARATH	Q9sna46 arabidopsis
748	193.5	6.2	574	2	Q3MIN2_HUMAN	Q3min2 homo sapien	821	189	6.0	1392	2	Q9VAD1_DROME	Q9vad1 drosophila
749	193.5	6.2	721	2	Q50W68_CABER	Q50w68 caenorhabdi	822	189	6.0	4311	2	Q7YOK5_CANFA	Q7yok5 canis famil
750	193.5	6.2	721	1	Y2082_MYCTU	Q10690 mycobacteri	823	188.5	6.0	348	2	Q32QV7_EPTST	Q32qv7 eptatretus
751	193.5	6.2	863	2	Q7TZ24_MYCBO	Q7tz24 mycobacteri	824	188.5	6.0	348	2	Q32QV7_EPTST	Q32qv7 eptatretus
752	193.5	6.2	863	2	Q4XA62_METBA	Q4xa62 methanosarc	825	188.5	6.0	369	2	Q6GM15_BRARE	Q6gm15 brachydanio
753	193.5	6.2	881	2	Q2XY24_DROSI	Q2xy24 drosophila	826	188.5	6.0	410	2	Q504E0_BRARE	Q504e0 brachydanio
754	193.5	6.2	881	2	Q2XY26_DROME	Q2xy26 drosophila	827	188.5	6.0	433	2	Q9DDZ7_PETMA	Q9ddz7 petromyzon
755	193.5	6.2	893	2	Q96C25_HUMAN	Q96c25 homo sapien	828	188.5	6.0	440	1	OMGP_MOUSE	Q53uv3 mus musculus
756	193.5	6.2	910	2	Q9HB75_HUMAN	Q9hb75 homo sapien	829	188.5	6.0	440	2	Q3UV73_MOUSE	Q3uv73 mus musculus
757	193.5	6.2	967	2	Q3UVD5_MOUSE	Q3uud5 mus musculus	830	188.5	6.0	538	2	Q5Z8W0_ORYZA	Q5z8w0 oryza sativ
758	193.5	6.2	977	1	SLIK3_HUMAN	Q94933 homo sapien	831	188.5	6.0	655	2	Q4SBU9_TETNG	Q4sbu9 tetraodon n
759	193.5	6.2	1333	2	Q2XXV8_DROSI	Q2xxv8 drosophila	832	188.5	6.0	677	2	Q3KR19_HUMAN	Q3kr19 homo sapien
760	193	6.2	252	2	Q4GL12_EPTST	Q4gl12 eptatretus	833	188	6.0	218	2	Q2VGY9_PETMA	Q2vgy9 petromyzon
761	193	6.2	319	2	Q32R40_EPTBU	Q32r40 eptatretus	834	188	6.0	324	2	Q32QR1_EPTST	Q32qr1 eptatretus



835	188	6.0	368	2	Q53HU6_HUMAN	Q53hu6 homo sapien	908	184	5.9	253	2	Q6E4K5_PETMA	Q6e4k5 petromyzon
836	188	6.0	369	1	PGS1_CANFA	O02678 canis famli	909	184	5.9	263	2	Q6E4K7_PETMA	Q6e4k7 petromyzon
837	188	6.0	369	2	Q3UXK8_MOUSE	O03xk8 mus musculus	910	184	5.9	274	2	Q4G1M0_EPTBU	Q4g1m0 eptatretus
838	188	6.0	369	2	Q7TWM3_MOUSE	O8k377 mus musculus	911	184	5.9	291	1	Q4RF21_TETNG	Q4rf21 tetraodon n
839	188	6.0	522	1	LRTM1_MOUSE	O8k377 mus musculus	912	184	5.9	368	1	PGS1_HUMAN	P21810 homo sapien
840	188	6.0	522	2	Q3UVX1_MOUSE	O3uxx1 mus musculus	913	184	5.9	368	2	Q53PF4_HUMAN	P21814 homo sapien
841	188	6.0	626	2	Q4SE92_TETNG	O4se92 tetraodon n	914	184	5.9	369	2	Q3TAF9_MOUSE	Q3taf9 mus musculus
842	188	6.0	818	2	Q5ZIH8_CHICK	O5zih8 gallus gall	915	184	5.9	473	2	Q7QF76_ANOGA	Q7qf76 anopheles g
843	187.5	6.0	195	2	Q2VGR5_PETMA	Q2vg10 eptatretus	916	184	5.9	543	2	Q4RGC6_TETNG	Q4rgc6 tetraodon n
844	187.5	6.0	259	2	Q4G1L0_EPTBU	O4g1l0 eptatretus	917	184	5.9	552	2	Q6K6X6_ORYSA	Q6k6x6 oryza sativ
845	187.5	6.0	310	2	Q9DDZ8_PETMA	O9ddz8 petromyzon	918	184	5.9	565	2	Q7PJD0_ANOGA	Q7pjd0 anopheles g
846	187.5	6.0	350	2	Q5M7S9_XENTR	O5m7s9 xenopus tro	919	184	5.9	837	1	SLIK4_MOUSE	Q8li08 mus musculus
847	187.5	6.0	352	2	Q4W6V7_CHICK	O4w6v7 gallus gall	920	184	5.9	1058	2	Q3MNF2_BOVIN	Q3mnf2 bos taurus
848	187.5	6.0	363	2	Q9H5G9_HUMAN	O9h5g9 homo sapien	921	183.5	5.9	187	2	Q6E4F6_PETMA	Q6e4f6 petromyzon
849	187.5	6.0	425	2	Q9VGH2_DROME	O9vgh2 drosophila	922	183.5	5.9	287	2	Q9W2B9_DROME	Q9w2b9 drosophila
850	187.5	6.0	601	1	LRC40_BRARE	Q7xsw3 brachydanio	923	183.5	5.9	292	2	Q6NYE6_BRARE	Q6ny6 brachydanio
851	187.5	6.0	861	2	Q4ZJ82_CHICK	O4zj82 gallus gall	924	183.5	5.9	652	2	Q7Q6Y6_ANOGA	Q7q6y6 anopheles g
852	187.5	6.0	885	2	Q2XY22_DROYA	O2xy22 drosophila	925	183.5	5.9	727	2	Q6A0E8_MOUSE	Q6a0e8 mus musculus
853	187	6.0	260	2	Q4G1K7_EPTST	O4g1k7 eptatretus	926	183.5	5.9	795	1	TLR1_MOUSE	Q9epq1 mus musculus
854	187	6.0	262	2	Q4G1K0_EPTST	O4g1k0 eptatretus	927	183.5	5.9	824	2	Q5GGX1_PIG	Q5ggx1 sus scrofa
855	187	6.0	324	2	Q2YE79_EPTST	O2ye79 eptatretus	928	183.5	5.9	841	1	TLR4_PIG	Q6hy56 sus scrofa
856	187	6.0	592	2	Q61PG4_CAEBR	O61pg4 caenorhabdi	929	183.5	5.9	841	2	Q401C7_PIG	Q401c7 sus scrofa
857	187	6.0	615	2	Q9VZ84_DROME	O9vz84 drosophila	930	183.5	5.9	864	2	Q2XY30_DROSI	Q2xy30 drosophila
858	187	6.0	735	2	Q6E114_MOUSE	O6e114 mus musculus	931	183.5	5.9	864	2	Q2XY31_DROSI	Q2xy31 drosophila
859	187	6.0	818	2	Q5WA51_CHICK	O5wa51 gallus gall	932	183.5	5.9	867	2	Q2XY27_DROER	Q2xy27 drosophila
860	187	6.0	1741	2	Q5LJU2_DROME	O5lju2 drosophila	933	183.5	5.9	871	2	Q2XY28_DROYA	Q2xy28 drosophila
861	186.5	5.9	193	2	Q2VHC4_PETMA	O2vhc4 petromyzon	934	183.5	5.9	871	2	Q2XY29_DROYA	Q2xy29 drosophila
862	186.5	5.9	323	2	Q32QV0_EPTST	O32qv0 eptatretus	935	183.5	5.9	1059	2	Q5ZJD0_CHICK	Q5zjd0 gallus gall
863	186.5	5.9	368	1	PGS1_XENLA	O9ib75 xenopus lae	936	183.5	5.9	1322	2	Q2M1B0_DROPS	Q2mb10 drosophila
864	186.5	5.9	521	2	Q72UJ4_LEPIC	O72uj4 leptospira	937	183.5	5.9	1537	1	LREC7_HUMAN	Q96nw7 homo sapien
865	186.5	5.9	639	2	Q5VZ17_HUMAN	O5vz17 homo sapien	938	183	5.8	432	2	Q8BJ03_MOUSE	Q8bj09 mus musculus
866	186.5	5.9	799	2	Q5VZ18_HUMAN	O5vz18 homo sapien	939	183	5.8	540	2	Q9VU53_DROME	Q9vu53 drosophila
867	186.5	5.9	839	1	TLR4_HUMAN	O00206 homo sapien	940	183	5.8	568	2	Q6P3Y9_MOUSE	Q6p3y9 mus musculus
868	186.5	5.9	839	1	TLR4_PANPA	O9ttn0 pan paniscu	941	183	5.8	662	1	LRC32_HUMAN	Q14392 homo sapien
869	186.5	5.9	839	2	Q5VZ19_HUMAN	O5vz19 homo sapien	942	183	5.8	664	2	Q7ZT81_ONCMY	Q7zt81 oncorhynch
870	186	5.9	216	2	Q2VGI9_PETMA	O2vgi9 petromyzon	943	183	5.8	972	2	Q5ZJ34_CHICK	Q5zj34 gallus gall
871	186	5.9	218	2	Q2VGR1_PETMA	O2vg14 petromyzon	944	182.5	5.8	187	2	Q6E4G1_PETMA	Q6e4g1 petromyzon
872	186	5.9	273	2	Q6E4B4_PETMA	O6e4b4 petromyzon	945	182.5	5.8	187	2	Q6E4G7_PETMA	Q6e4g7 petromyzon
873	186	5.9	368	2	Q5RAY4_PONPY	O5ray4 pongo pygma	946	182.5	5.8	219	2	Q2VGV7_PETMA	Q2vgv7 petromyzon
874	186	5.9	440	1	OMGP_HUMAN	P23515 homo sapien	947	182.5	5.8	257	2	Q4G1L8_EPTBU	Q4g1l8 eptatretus
875	186	5.9	440	2	Q53H88_HUMAN	Q53hb8 homo sapien	948	182.5	5.8	261	2	Q2YB27_EPTBU	Q2ye27 eptatretus
876	186	5.9	552	2	Q9VT44_DROME	O9vt44 drosophila	949	182.5	5.8	298	2	Q32QV7_EPTBU	Q32qv7 eptatretus
877	186	5.9	623	1	LRC21_HUMAN	O9p2v4 homo sapien	950	182.5	5.8	379	1	ASPN_HUMAN	Q9bxx1 homo sapien
878	186	5.9	1029	1	TLR9_BOVIN	O512m5 bos taurus	951	182.5	5.8	380	2	Q5TBF3_HUMAN	Q5tbf3 homo sapien
879	185.5	5.9	185	2	Q2VGV1_PETMA	O2vgv1 petromyzon	952	182.5	5.8	384	2	Q6P528_HUMAN	Q6p528 homo sapien
880	185.5	5.9	191	2	Q2VGC6_PETMA	O2vgc6 petromyzon	953	182.5	5.8	810	2	Q8T3J2_DROME	Q8t3j2 drosophila
881	185.5	5.9	191	2	Q2VGR0_PETMA	O2vg10 petromyzon	954	182.5	5.8	811	2	Q9VK54_DROME	Q9vk54 drosophila
882	185.5	5.9	191	2	Q2VGT6_PETMA	O2vgc6 petromyzon	955	182.5	5.8	828	1	TLR4_PONPY	Q8spe9 pongo pygma
883	185.5	5.9	195	2	Q2VXK9_PETMA	O2vgx9 petromyzon	956	182.5	5.8	837	1	TLR4_GORGO	Q8spe8 gorilla gor
884	185.5	5.9	251	2	Q2VE24_EPTST	O2ve24 eptatretus	957	182.5	5.8	864	2	Q2XY32_DROME	Q2xy32 drosophila
885	185.5	5.9	369	2	Q4T3M1_TETNG	O4t3m1 tetraodon n	958	182.5	5.8	880	2	P91643_DROME	P91643 drosophila
886	185.5	5.9	466	2	Q661W3_XENLA	O661w3 xenopus lae	959	182.5	5.8	958	1	SLIK5_HUMAN	Q94991 homo sapien
887	185.5	5.9	953	2	Q6MF87_PARUW	O6mf87 parachlamyd	960	182.5	5.8	958	2	Q4QOHI_HUMAN	Q4qohi homo sapien
888	185	5.9	254	2	Q4S4N7_TETNG	O4s4n7 tetraodon n	961	182.5	5.8	958	2	Q5VT81_HUMAN	Q5vt81 homo sapien
889	185	5.9	323	2	Q32R21_EPTBU	Q32r21 eptatretus	962	182.5	5.8	1041	2	Q3HJ14_TRIER	Q3hj14 trichodesmi
890	185	5.9	389	2	Q6BP51_BRARE	O6bp51 brachydanio	963	182	5.8	192	2	Q2VGF9_PETMA	Q2vgf9 petromyzon
891	185	5.9	512	2	Q6PEZ8_HUMAN	O6pez8 homo sapien	964	182	5.8	194	2	Q2VGZ0_PETMA	Q2vgz0 petromyzon
892	185	5.9	603	1	LRC40_CHICK	O5zln0 gallus gall	965	182	5.8	205	2	Q4B9X7_TETNG	Q4b9x7 tetraodon n
893	184.5	5.9	257	2	Q4G1L5_EPTBU	O4g1l5 eptatretus	966	182	5.8	252	2	Q4G1L8_EPTST	Q4g1l8 eptatretus
894	184.5	5.9	259	2	Q2YE09_EPTST	O2ye09 eptatretus	967	182	5.8	271	2	Q6E4C4_PETMA	Q6e4c4 petromyzon
895	184.5	5.9	270	2	Q4KP09_LAMAP	O4kp09 lampetra ap	968	182	5.8	297	2	Q6E4C4_PETMA	Q6e4c4 petromyzon
896	184.5	5.9	724	2	Q5XWB9_HORSE	O5xwb9 equus cabal	969	182	5.8	319	2	Q32R34_EPTBU	Q32r34 eptatretus
897	184.5	5.9	799	2	Q9V964_DROME	O9v964 drosophila	970	182	5.8	369	1	PGS1_SHEEP	Q64390 ovis aries
898	184.5	5.9	839	2	Q6R2V6_MOUSE	O6r2v6 mus musculus	971	182	5.8	369	2	Q5BIM3_BOVIN	Q5bim3 bos taurus
899	184.5	5.9	841	2	Q2TNK4_PIG	O2tnk4 sus scrofa	972	182	5.8	373	2	Q5B145_BRARE	Q5b145 brachydanio
900	184.5	5.9	841	2	Q5F4K7_PIG	O5f4k7 sus scrofa	973	182	5.8	373	2	Q803T7_BRARE	Q803t1 brachydanio
901	184.5	5.9	843	1	TLR4_HORSE	O9myw3 equus cabal	974	182	5.8	428	2	Q8F3F8_LEPIN	Q8f3f8 leptospira
902	184.5	5.9	957	1	SLIK5_MOUSE	O810b7 mus musculus	975	182	5.8	532	2	O96671_DROME	O96671 drosophila
903	184.5	5.9	1007	2	Q65XS3_ORYSA	Q65xs3 oryza sativ	976	182	5.8	678	2	Q7Q550_ANOGA	Q7q550 anopheles g
904	184.5	5.9	1046	2	Q5G097_CHICK	O5gg97 gallus gall	977	182	5.8	1022	2	O8HXV0_BOVIN	Q8hxxv0 bos taurus
905	184.5	5.9	1214	2	Q69JN6_ORYSA	Q69jn6 oryza sativ	978	182	5.8	1029	2	O866B2_BOVIN	Q866b2 bos taurus
906	184	5.9	187	2	Q6E4M5_PETMA	Q6e4m5 petromyzon	979	181.5	5.8	180	2	Q8BPJ0_MOUSE	Q8bpj0 mus musculus
907	184	5.9	192	2	Q2VGJ6_PETMA	Q2vgj6 petromyzon	980	181.5	5.8	185	2	Q2VGZ9_PETMA	Q2vgz9 petromyzon



981	181.5	5.8	191	2	Q2VH42_PETMA	Q2vh42	petromyzon	1054	178	5.7	298	2	Q32OX4_EPTST	Q32qx4	eptaretus
982	181.5	5.8	251	2	Q4G1K2_EPTST	Q4g1k2	eptaretus	1055	178	5.7	319	2	Q32QZ3_EPTBU	Q32qz3	eptaretus
983	181.5	5.8	259	2	Q4G1J8_EPTST	Q4g1j8	eptaretus	1056	178	5.7	364	2	Q66J59_XENLA	Q66j59	xenopus lae
984	181.5	5.8	298	2	Q32R41_EPTBU	Q32r41	eptaretus	1057	178	5.7	391	2	Q4RQ11_TETNG	Q4rq11	tetraodon n
985	181.5	5.8	357	1	PGS2_CHICK	P28675	gallus gall	1058	178	5.7	488	2	Q4RXQ5_TETNG	Q4rxq5	tetraodon n
986	181.5	5.8	599	2	Q7T3H6_BRARE	P273h6	brachydanio	1059	178	5.7	522	1	LRTM1_HUMAN	Q86ue6	homo sapien
987	181.5	5.8	699	2	Q61PG3_CAERB	Q61pg3	caenorhabdi	1060	178	5.7	894	2	Q9BJD6_STRPU	Q86jd6	strongyloce
988	181.5	5.8	2160	2	Q13328_MAGGR	Q13328	magnaporthe	1061	178	5.7	1049	1	TLR7_HUMAN	Q9nyk1	homo sapien
989	181.5	5.8	2160	2	Q13488_MAGGR	Q13488	magnaporthe	1062	178	5.7	1052	2	Q9Y4C4_HUMAN	Q9y4c4	homo sapien
990	181	5.8	192	2	Q2VGY4_PETMA	Q2vgy4	petromyzon	1063	178	5.7	1257	2	Q2VFN8_ANOGA	Q2vfn8	anopheles g
991	181	5.8	298	2	Q2YB69_EPTST	Q2yb69	eptaretus	1064	177.5	5.7	187	2	Q2VH41_PETMA	Q2vh41	petromyzon
992	181	5.8	372	1	PGS1_HORSE	Q46403	equus cabal	1065	177.5	5.7	195	2	Q2VGD7_PETMA	Q2vgd7	petromyzon
993	181	5.8	569	2	Q7Q1F3_ANOGA	Q7q1f3	anopheles g	1066	177.5	5.7	215	2	Q2VGS6_PETMA	Q2vgs6	petromyzon
994	181	5.8	1013	2	Q8LQ10_ORYSA	Q8lq10	oryza sativ	1067	177.5	5.7	275	2	Q4G1K5_EPTST	Q4g1k5	eptaretus
995	181	5.8	1333	2	Q7Q168_ANOGA	Q7q168	anopheles g	1068	177.5	5.7	796	2	Q4LDR7_PIG	Q4ldr7	sus scrofa
996	180.5	5.8	371	2	Q6GLQ6_XENLA	Q6glq6	xenopus lae	1069	177.5	5.7	796	2	Q59H19_PIG	Q59h19	sus scrofa
997	180.5	5.8	385	2	Q8BMW6_MOUSE	Q8bmw6	mus musculus	1070	177.5	5.7	809	2	Q4RMQ1_TETNG	Q4rmq1	tetraodon n
998	180.5	5.8	441	2	Q81170_DROVI	Q81170	drosohila	1071	177.5	5.7	1026	2	Q5SMW2_ORYSA	Q5smw2	oryza sativ
999	180.5	5.8	522	1	AMGO2_FONPY	Q5r7m3	pongo pygma	1072	177.5	5.7	1050	1	TLR7_MOUSE	P58681	mus musculus
1000	180.5	5.8	584	2	Q6PGX3_BRARE	Q6pgx3	brachydanio	1073	177.5	5.7	1050	2	Q548J0_MOUSE	Q548j0	m toll-like
1001	180.5	5.8	821	2	Q96PY3_HUMAN	Q96py3	homo sapien	1074	177.5	5.7	1360	2	Q7KTA0_DROME	Q7kca0	drosohila
1002	180.5	5.8	1443	2	Q9VJQ0_DROME	Q9vjq0	drosohila	1075	177.5	5.7	2300	1	CYAA_NEUTRA	Q01631	neurospora
1003	180.5	5.8	1460	2	Q5H261_XENTR	Q5h261	xenopus tro	1076	177.5	5.7	2493	1	CYAA_NEUTRA	P49606	ustilago ma
1004	180	5.7	192	2	Q2VH29_PETMA	Q2vh29	petromyzon	1077	177.5	5.7	2493	2	Q4P3T1_USTMA	Q4p3t1	ustilago ma
1005	180	5.7	250	2	Q4G1M2_EPTBU	Q4g1m2	eptaretus	1078	177	5.6	187	2	Q6B4H5_PETMA	Q6ebh5	petromyzon
1006	180	5.7	369	1	PGS1_BOVIN	F21809	bos taurus	1079	177	5.6	192	2	Q2VGO0_PETMA	Q2vg00	petromyzon
1007	180	5.7	522	1	LRTM1_PONPY	Q5r6b1	pongo pygma	1080	177	5.6	192	2	Q2VGR6_PETMA	Q2vgr6	petromyzon
1008	180	5.7	817	2	Q86P15_DROME	Q86p15	drosohila	1081	177	5.6	192	2	Q2VGM2_PETMA	Q2vgm2	petromyzon
1009	180	5.7	817	2	Q9VS84_DROME	Q9vs84	drosohila	1082	177	5.6	192	2	Q2VH26_PETMA	Q2vh26	petromyzon
1010	180	5.7	843	2	Q7ZTG5_CHICK	Q7ztg5	gallus gall	1083	177	5.6	192	2	Q2VH28_PETMA	Q2vh28	petromyzon
1011	180	5.7	869	2	Q4S0C1_TETNG	Q4s0c1	tetraodon n	1084	177	5.6	334	2	Q4SBU8_TETNG	Q4sbu8	tetraodon n
1012	179.5	5.7	185	2	Q2VGI7_PETMA	Q2vgi7	petromyzon	1085	177	5.6	343	1	LUM_COTJA	Q9de67	coturnix co
1013	179.5	5.7	187	2	Q6E4D6_PETMA	Q6e4d6	petromyzon	1086	177	5.6	347	2	Q58A48_BRARE	Q58a48	brachydanio
1014	179.5	5.7	195	2	Q2VGP4_PETMA	Q2vgp4	petromyzon	1087	177	5.6	662	1	LRC32_PONPY	Q5r101	pongo pygma
1015	179.5	5.7	585	2	Q61GX3_CAERB	Q61gx3	caenorhabdi	1088	177	5.6	666	2	Q7Q2W6_ANOGA	Q7q2w6	anopheles g
1016	179.5	5.7	799	2	Q3BBY2_MACMU	Q3bby2	macaca mula	1089	177	5.6	670	2	Q5FW85_MOUSE	Q5fw85	m adult mal
1017	179.5	5.7	820	2	Q5R3F8_HUMAN	Q5r3f8	homo sapien	1090	177	5.6	1370	2	Q58NA4_APTME	Q58na4	apis mellif
1018	179.5	5.7	1117	1	LRI3G_MOUSE	Q6pic6	mus musculus	1091	176.5	5.6	185	2	Q2VGE5_PETMA	Q2vge5	petromyzon
1019	179.5	5.7	4283	2	Q9ERV0_RAT	Q9erv0	rattus norv	1092	176.5	5.6	187	2	Q6E4M0_PETMA	Q6em40	petromyzon
1020	179	5.7	192	2	Q2VGC7_PETMA	Q2vgc7	petromyzon	1093	176.5	5.6	195	2	Q2VGT9_PETMA	Q2vgt9	petromyzon
1021	179	5.7	192	2	Q2VG8_PETMA	Q2vg8	petromyzon	1094	176.5	5.6	322	2	Q32R02_EPTBU	Q32r02	eptaretus
1022	179	5.7	192	2	Q2VH01_PETMA	Q2vh01	petromyzon	1095	176.5	5.6	520	2	Q5VR46_ORYSA	Q5vr46	oryza sativ
1023	179	5.7	194	2	Q2VH46_PETMA	Q2vh46	petromyzon	1096	176.5	5.6	522	1	AMGO2_HUMAN	Q86sj2	homo sapien
1024	179	5.7	262	2	Q2YELL_EPTST	Q2yell	eptaretus	1097	176.5	5.6	522	2	Q4VBP6_HUMAN	Q4vbp6	homo sapien
1025	179	5.7	273	2	Q6E4B8_PETMA	Q6e4b8	petromyzon	1098	176.5	5.6	628	2	Q7PVZ6_ANOGA	Q7pvz6	anopheles g
1026	179	5.7	314	1	LRC52_MOUSE	Q5m8m9	mus musculus	1099	176.5	5.6	856	2	Q59H17_PIG	Q59h17	sus scrofa
1027	179	5.7	534	2	Q9VT85_DROME	Q9vt89	drosohila	1100	176.5	5.6	901	2	Q4SBD4_TETNG	Q4sbd4	tetraodon n
1028	179	5.7	700	2	Q9P244_HUMAN	Q9p244	homo sapien	1101	176.5	5.6	1495	1	LRRC7_RAT	P70587	rattus norv
1029	179	5.7	742	2	Q9BJD4_STRPU	Q9bjd4	strongyloce	1102	176.5	5.6	1756	2	Q6AWK8_DROME	Q6awk8	drosohila
1030	179	5.7	751	2	Q2QP46_ORYSA	Q2qp46	oryza sativ	1103	176	5.6	220	2	Q2VH09_PETMA	Q2vh09	petromyzon
1031	179	5.7	905	1	TLR3_MOUSE	Q99mb1	mus musculus	1104	176	5.6	249	2	Q4SUM4_TETNG	Q4sum4	tetraodon n
1032	179	5.7	905	2	Q499F3_MOUSE	Q499f3	mus musculus	1105	176	5.6	503	2	Q8LJ87_ORYSA	Q8lj87	oryza sativ
1033	179	5.7	969	2	Q4LBC9_ONCMY	Q4lbc9	oncorhynch	1106	176	5.6	623	2	Q95S21_DROME	Q95s21	drosohila
1034	179	5.7	1029	1	TLR9_SHEEP	Q5i2m4	ovis aries	1107	176	5.6	862	2	Q5GR02_CHICK	Q5gr02	gallus gall
1035	178.5	5.7	161	2	Q2VH51_PETMA	Q2vh51	petromyzon	1108	176	5.6	904	2	Q5TJ59_BOVIN	Q5tj59	bos taurus
1036	178.5	5.7	176	2	Q567L5_BRARE	Q567l5	brachydanio	1109	176	5.6	905	2	Q5TJ58_BOVIN	Q5tj58	bos taurus
1037	178.5	5.7	190	2	Q6E4D8_PETMA	Q6e4d8	petromyzon	1110	176	5.6	906	2	Q4SRZ0_TETNG	Q4srz0	tetraodon n
1038	178.5	5.7	348	2	Q5R143_BRARE	Q5r143	brachydanio	1111	176	5.6	1032	1	TLR9_CANFA	Q5i2m8	canis fami
1039	178.5	5.7	356	1	PGS2_COTJA	Q9dec8	coturnix co	1112	176	5.6	1257	2	Q9VK28_DROME	Q9vk28	drosohila
1040	178.5	5.7	443	2	Q67VV7_ORYSA	Q67vv7	oryza sativ	1113	176	5.6	1412	1	LAP2_HUMAN	Q96rt1	homo sapien
1041	178.5	5.7	493	1	AMG01_HUMAN	Q66wk6	homo sapien	1114	175.5	5.6	167	2	Q2VGJ8_PETMA	Q2vgj8	petromyzon
1042	178.5	5.7	587	2	Q4QGJ9_LEIMA	Q4qgj9	leishmania	1115	175.5	5.6	185	2	Q2VGN3_PETMA	Q2vgn3	petromyzon
1043	178.5	5.7	1024	1	POPC_RALSO	Q9rb2	ralstonia s	1116	175.5	5.6	251	2	Q2YE03_EPTST	Q2ye03	eptaretus
1044	178.5	5.7	1063	2	Q5Z666_ORYSA	Q5z666	oryza sativ	1117	175.5	5.6	272	2	Q4KEP14_PETTR	Q4kep14	ichthyomyzo
1045	178.5	5.7	1104	2	Q7XUH4_ORYSA	Q7xuh4	oryza sativ	1118	175.5	5.6	324	2	Q32R05_EPTBU	Q32r05	eptaretus
1046	178.5	5.7	1107	2	Q3MD20_ANAVT	Q3md20	anaabaena va	1119	175.5	5.6	384	2	Q4T0V4_TETNG	Q4t0v4	tetraodon n
1047	178.5	5.7	1310	1	GP125_MOUSE	Q7t36	mus musculus	1120	175.5	5.6	440	2	Q7TNM3_RAT	Q7tnm3	rattus norv
1048	178	5.7	187	2	Q6E4H4_PETMA	Q6e4h4	petromyzon	1121	175.5	5.6	492	1	AMG01_MOUSE	Q80z38	mus musculus
1049	178	5.7	192	2	Q2VH53_PETMA	Q2vh53	petromyzon	1122	175.5	5.6	841	2	Q2V898_BOSTR	Q2v898	boselaphus
1050	178	5.7	192	2	Q2VH56_PETMA	Q2vh56	petromyzon	1123	175.5	5.6	1017	2	Q5H718_FUGRU	Q5h718	fugu rubrip
1051	178	5.7	194	2	Q2VGE4_PETMA	Q2vge4	petromyzon	1124	175.5	5.6	1490	1	LRRC7_MOUSE	Q80t67	mus musculus
1052	178	5.7	231	2	Q3TV01_MOUSE	Q3tv01	mus musculus	1125	175.5	5.6	1731	2	Q4SOD3_TETNG	Q4sod3	tetraodon n
1053	178	5.7	296	2	Q32QX9_EPTST	Q32qx9	eptaretus	1126	175	5.6	168	2	Q2VHC0_PETMA	Q2vhc0	petromyzon



1127	175	5.6	192	2	Q2VGK6_PETMA	Q2vgk6 petromyzon	1200	172.5	5.5	378	2	Q5R294_DROSI	Q5r294 drosophila
1128	175	5.6	192	2	Q2VH74_PETMA	Q2vh74 petromyzon	1201	172.5	5.5	739	2	Q60NV9_CAEBR	Q60nv9 caenorhabdi
1129	175	5.6	252	2	Q4GIJ2_EPTST	Q4gij2 eptatretus	1202	172.5	5.5	823	2	Q68FM6_MOUSE	Q68fm6 mus musculus
1130	175	5.6	297	2	Q32O20_EPTBU	Q32o20 eptatretus	1203	172.5	5.5	823	2	Q8CCW8_MOUSE	Q8ccw8 mus musculus
1131	175	5.6	323	2	Q32O20_EPTBU	Q32o20 eptatretus	1204	172.5	5.5	1711	2	Q59DT7_DROME	Q59dt7 drosophila
1132	175	5.6	343	1	LUM_CHICK	P51890 gallus gall	1205	172.5	5.5	1850	2	Q59DT8_DROME	Q59dt8 drosophila
1133	175	5.6	510	2	Q9BGY6_MACFA	Q9bgy6 macaca fasc	1206	172.5	5.5	1851	1	LAM4_DROME	Q7k1y7 drosophila
1134	175	5.6	905	2	Q3TM31_MOUSE	Q3tm31 mus musculus	1207	172.5	5.5	4256	2	Q8MJF3_CANPA	Q8mjf3 canis famli
1135	175	5.6	941	2	Q5H722_FUGRU	Q5h722 fugu rubrip	1208	172	5.5	339	2	Q4SU68_TETNG	Q4su68 tetraodon n
1136	175	5.6	973	2	Q6KCC7_ONCWY	Q6kcc7 oncorhynch	1209	172	5.5	347	2	Q72UT1_BRARE	Q72ut1 brachydanio
1137	175	5.6	1137	2	Q7QHH1_ANOGA	Q7qhh1 anopheles g	1210	172	5.5	411	2	Q4S9P3_TETNG	Q4s9p3 tetraodon n
1138	174.5	5.6	130	2	Q6E4E5_PETMA	Q6e4e5 petromyzon	1211	172	5.5	577	2	Q8N3K5_HUMAN	Q8n3k5 homo sapien
1139	174.5	5.6	191	2	Q2VGI5_PETMA	Q2vgi5 petromyzon	1212	172	5.5	1134	2	Q6S510_ARATH	Q6s510 arabidopsis
1140	174.5	5.6	193	2	Q2VGDO_PETMA	Q2vgdo petromyzon	1213	172	5.5	1693	2	Q4INH4_GIBZE	Q4inh4 gibberella
1141	174.5	5.6	440	2	Q4J5V4_AZOV1	Q4j5v4 azotobacter	1214	171.5	5.5	171	2	Q2VGJ0_PETMA	Q2vgj0 petromyzon
1142	174.5	5.6	512	2	Q9CQ76_MOUSE	Q9cq76 m 8 days em	1215	171.5	5.5	193	2	Q2VHD1_PETMA	Q2vhd1 petromyzon
1143	174.5	5.6	567	2	Q4SL10_TETNG	Q4sl10 tetraodon n	1216	171.5	5.5	195	2	Q2VH57_PETMA	Q2vh57 petromyzon
1144	174.5	5.6	602	1	LRC40_MOUSE	Q9cnc8 mus musculus	1217	171.5	5.5	378	2	Q9V900_DROME	Q9v900 drosophila
1145	174.5	5.6	605	1	LRC40_XENLA	Q6gpj5 xenopus lae	1218	171.5	5.5	605	1	LRC40_XENR	Q5m8g4 xenopus tro
1146	174.5	5.6	795	1	TLR6_MOUSE	Q9epw9 mus musculus	1219	171.5	5.5	683	1	LRC44_HUMAN	Q75427 homo sapien
1147	174.5	5.6	806	2	Q3UV88_MOUSE	Q3uv88 mus musculus	1220	171.5	5.5	791	2	Q2L8H0_LISMO	Q2l8h0 listeria mo
1148	174.5	5.6	1020	2	Q5ZED4_ORYSA	Q5zed4 oryza sativ	1221	171.5	5.5	858	1	LRC8D_RAT	Q2l8h0 listeria mo
1149	174.5	5.6	1060	2	Q6ZGM3_ORYSA	Q6zgm3 oryza sativ	1222	171.5	5.5	858	1	TLR5_HUMAN	Q60602 homo sapien
1150	174	5.6	194	2	Q2VH35_PETMA	Q2vh35 petromyzon	1223	171.5	5.5	858	2	Q32MI2_HUMAN	Q32mi2 homo sapien
1151	174	5.6	196	2	Q2VGF0_PETMA	Q2vgf0 petromyzon	1224	171.5	5.5	858	2	Q32MI3_HUMAN	Q32mi3 homo sapien
1152	174	5.6	299	2	Q32R28_EPTBU	Q32r28 eptatretus	1225	171.5	5.5	859	1	LRC8D_MOUSE	Q8bgr2 mus musculus
1153	174	5.6	490	2	Q4RYL5_TETNG	Q4ryl5 tetraodon n	1226	171.5	5.5	859	2	Q3T170_MOUSE	Q3t170 mus musculus
1154	174	5.6	535	2	Q8RX50_BRANI	Q8rx50 brassica ni	1227	171.5	5.5	859	2	Q3UVA9_MOUSE	Q3uva9 mus musculus
1155	174	5.6	544	2	Q7Q2W5_ANOGA	Q7q2w5 anopheles g	1228	171.5	5.5	1589	2	Q9UJU9_METAN	Q9uuq9 metarhizium
1156	174	5.6	651	2	Q4JQO2_XENLA	Q4jqo2 xenopus lae	1229	171	5.5	168	2	Q2VHF6_PETMA	Q2vhf6 petromyzon
1157	174	5.6	859	1	TLR5_MOUSE	Q9jlf7 mus musculus	1230	171	5.5	192	2	Q2VGZ1_PETMA	Q2vgz1 petromyzon
1158	174	5.6	913	2	Q3KUR8_ONCWY	Q3kur8 oncorhynch	1231	171	5.5	194	2	Q2VGS3_PETMA	Q2vgs3 petromyzon
1159	174	5.6	951	1	LGR4_RAT	Q9z2h4 rattus norv	1232	171	5.5	299	2	Q32QZ7_EPTBU	Q32qz7 eptatretus
1160	173.5	5.5	161	2	Q2VH22_PETMA	Q2vh22 petromyzon	1233	171	5.5	354	2	Q3TSV1_MOUSE	Q3tsv1 mus musculus
1161	173.5	5.5	261	2	Q5MBT1_HUMAN	Q5mbt1 homo sapien	1234	171	5.5	360	1	PGS2_PIG	Q9xsd9 sus scrofa
1162	173.5	5.5	337	2	Q4RXJ0_TETNG	Q4rxj0 tetraodon n	1235	171	5.5	360	1	Q6DV11_GECJA	Q6dv11 gecko japon
1163	173.5	5.5	353	2	Q64OB1_XENR	Q64ob1 xenopus tro	1236	171	5.5	469	2	Q3URB9_MOUSE	Q3urb9 mus musculus
1164	173.5	5.5	364	2	Q6GNX8_XENLA	Q6gnx8 xenopus lae	1237	171	5.5	643	2	Q502J4_BRARE	Q502j4 brachydanio
1165	173.5	5.5	421	1	OMD_HUMAN	Q99983 homo sapien	1238	171	5.5	833	1	TLR4_FELCA	P58727 felis silve
1166	173.5	5.5	421	2	Q5TBF4_HUMAN	Q5tbf4 homo sapien	1239	171	5.5	976	2	Q3TAN2_MOUSE	Q3tan2 mus musculus
1167	173.5	5.5	440	2	Q7TQ25_RAT	Q7tq25 rattus norv	1240	171	5.5	976	2	Q3V1N1_MOUSE	Q3v1n1 mus musculus
1168	173.5	5.5	537	1	LG14_MOUSE	Q8k1s1 mus musculus	1241	171	5.5	1317	2	Q5TUS9_ANOGA	Q5tus9 anopheles g
1169	173.5	5.5	537	2	Q3UYI9_MOUSE	Q3uyi9 mus musculus	1242	170.5	5.4	185	2	Q2VGH0_PETMA	Q2vgh0 petromyzon
1170	173.5	5.5	727	2	Q6GV21_BOVIN	Q6gv21 bos taurus	1243	170.5	5.4	246	2	Q6E4J1_PETMA	Q6e4j1 petromyzon
1171	173.5	5.5	806	2	Q7TPC5_MOUSE	Q7tpc5 mus musculus	1244	170.5	5.4	359	2	Q4R5D2_MACFA	Q4r5d2 macaca fasc
1172	173.5	5.5	826	1	TLR4_PAPAN	Q9tsp2 papio anubi	1245	170.5	5.4	373	1	ASPN_MOUSE	Q99mg4 mus musculus
1173	173.5	5.5	884	2	Q5H720_FUGRU	Q5h720 fugu rubrip	1246	170.5	5.4	741	2	Q8KTF7_LISMO	Q8ktf7 listeria mo
1174	173	5.5	168	2	Q2VGX8_PETMA	Q2vgx8 petromyzon	1247	170.5	5.4	761	2	Q3XNG0_9PROT	Q3xng0 magnetococc
1175	173	5.5	192	2	Q2VGG5_PETMA	Q2vgs5 petromyzon	1248	170.5	5.4	794	2	Q2L8H9_LISMO	Q2l8h9 listeria mo
1176	173	5.5	192	2	Q2VHAC_PETMA	Q2vha2 petromyzon	1249	170.5	5.4	1031	1	TLR9_FELCA	Q015m7 felis silve
1177	173	5.5	194	2	Q2VHC8_PETMA	Q2vhc8 petromyzon	1250	170.5	5.4	2145	1	CYAA_PODAN	Q01513 podospora a
1178	173	5.5	252	2	Q6G1I4_EPTST	Q6g1i4 eptatretus	1251	170	5.4	187	2	Q6E4D9_PETMA	Q6e4d9 petromyzon
1179	173	5.5	269	2	Q6E4C2_PETMA	Q6e4c2 petromyzon	1252	170	5.4	192	2	Q2VGG2_PETMA	Q2vgg2 petromyzon
1180	173	5.5	360	1	PGS2_HORSE	Q46542 equus caball	1253	170	5.4	192	2	Q2VGI3_PETMA	Q2vgi3 petromyzon
1181	173	5.5	470	2	Q9V354_DROME	Q9v354 drosophila	1254	170	5.4	192	2	Q2VGM4_PETMA	Q2vgm4 petromyzon
1182	173	5.5	539	2	Q5O3F6_BRARE	Q5o3f6 brachydanio	1255	170	5.4	192	2	Q2VH20_PETMA	Q2vh20 petromyzon
1183	173	5.5	664	2	Q5UT54_SALSA	Q5ut54 salmo salar	1256	170	5.4	364	1	LRC19_MOUSE	Q8bzt5 mus musculus
1184	173	5.5	853	2	Q8CB40_MOUSE	Q8cb40 mus musculus	1257	170	5.4	473	2	Q3TSO3_MOUSE	Q3tsq3 mus musculus
1185	173	5.5	892	2	Q466H0_METEA	Q466h0 methanosarc	1258	170	5.4	572	2	Q4QGJ6_LEIMA	Q4qgj6 leishmania
1186	173	5.5	925	1	GLHR_ATEL	P35409 anthopieura	1259	170	5.4	883	2	Q4VAM0_HUMAN	Q4vam0 homo sapien
1187	173	5.5	1459	2	Q7QOC5_ANOGA	Q7qoc5 anopheles g	1260	170	5.4	907	1	LGR5_HUMAN	Q75473 homo sapien
1188	173	5.5	1459	2	Q8WR64_ANOGA	Q8wr64 anopheles g	1261	170	5.4	907	2	Q4VAM2_HUMAN	Q4vam2 homo sapien
1189	172.5	5.5	161	2	Q2VGH1_PETMA	Q2vgh1 petromyzon	1262	170	5.4	1024	2	Q84IE6_RALSO	Q84ie6 ralstonia s
1190	172.5	5.5	161	2	Q2VHB2_PETMA	Q2vhb2 petromyzon	1263	170	5.4	1032	2	Q59ER8_HUMAN	Q59er8 homo sapien
1191	172.5	5.5	163	2	Q6E4E2_PETMA	Q6e4e2 petromyzon	1264	169.5	5.4	167	2	Q2VGL5_PETMA	Q2vgld5 petromyzon
1192	172.5	5.5	171	2	Q2VHC2_PETMA	Q2vhc2 petromyzon	1265	169.5	5.4	173	2	Q2VGD2_PETMA	Q2vgd2 petromyzon
1193	172.5	5.5	237	2	Q2YEL3_EPTST	Q2yel3 eptatretus	1266	169.5	5.4	352	1	KERA_BOVIN	Q68x06 bos taurus
1194	172.5	5.5	259	2	Q2YER2_EPTST	Q2yer2 eptatretus	1267	169.5	5.4	366	2	Q8BX06_MOUSE	Q8bx06 mus musculus
1195	172.5	5.5	353	1	KERA_CHICK	Q42235 gallus gall	1268	169.5	5.4	463	2	Q2LYW7_DROPS	Q2lyw7 drosophila
1196	172.5	5.5	353	1	KERA_COTJA	Q9de66 coturnix co	1269	169.5	5.4	493	1	AMG01_RAT	Q80zd7 rattus norv
1197	172.5	5.5	359	1	PGS2_HUMAN	P07585 homo sapien	1270	169.5	5.4	651	2	Q4T8T9_TETNG	Q4t8t9 tetraodon n
1198	172.5	5.5	359	1	PGS2_PANTR	Q5riy9 pan troglod	1271	169.5	5.4	760	2	Q9TOK3_ARATH	Q9tok3 arabidopsis
1199	172.5	5.5	359	2	Q6FH10_HUMAN	Q6fh10 homo sapien	1272	169.5	5.4	876	2	Q67WE5_ORYSA	Q67we5 oryza sativ



1273	169.5	5.4	991	1	TLRL3_MOUSE	Q6r5n8	mus musculus
1274	169.5	5.4	1271	1	FLII_MOUSE	Q9jj28	mus musculus
1275	169	5.4	168	2	Q2VGQ9_PETMA	Q2vgg9	petromyzon
1276	169	5.4	217	2	Q66WJ6_FELCA	Q66wj6	felis silve
1277	169	5.4	273	2	Q5XPY6 ICTALURUS p	Q5xpy6	ictalurus p
1278	169	5.4	279	2	Q58HK2_TRASC	Q58hk2	trachemys s
1279	169	5.4	354	1	PGS2_MOUSE	P28G54	mus musculus
1280	169	5.4	354	1	Q3UKR1_MOUSE	Q3ukr1	m 14 days p
1281	169	5.4	360	2	Q6J0Y6_PAROL	Q6j0y6	paralichthys
1282	169	5.4	757	2	Q69MS7_ORYSA	Q69ms7	oryza sativ
1283	169	5.4	839	2	Q9RX57_DEIRA	Q9rx57	deinococcus
1284	169	5.4	1175	2	Q4RER3_TETNG	Q4rer3	tetraodon n
1285	169	5.4	1298	2	Q624K5_CABER	Q624k5	caenorhabdi
1286	169	5.4	1658	2	Q4PLE9_GIBIN	Q4ple9	gibberella
1287	168.5	5.4	169	2	Q2VH97_PETMA	Q2vh97	petromyzon
1288	168.5	5.4	184	2	Q2VGY2_PETMA	Q2vgy2	petromyzon
1289	168.5	5.4	246	2	Q2VGQ5_PETMA	Q2vgq5	petromyzon
1290	168.5	5.4	246	2	Q4KP10_LAMAP	Q4kp10	lampetra ap
1291	168.5	5.4	255	2	Q66WJ3_FELCA	Q66wj3	felis silve
1292	168.5	5.4	333	2	Q4SY28_TETNG	Q4sy28	tetraodon n
1293	168.5	5.4	343	2	Q501S3_BRARE	Q501s3	brachydanio
1294	168.5	5.4	353	2	Q7SYS8_XENLA	Q7sys8	xenopus lae
1295	168.5	5.4	363	2	Q8C9A7_MOUSE	Q8c9a7	mus musculus
1296	168.5	5.4	366	2	Q3UGP9_MOUSE	Q3ugp9	mus musculus
1297	168.5	5.4	378	2	Q5R264_DROSE	Q5r264	drosophila
1298	168.5	5.4	619	2	Q6R8K0_ORYSA	Q6r8k0	oryza sativ
1299	168.5	5.4	685	2	Q6T545_LISMO	Q6t545	listeria mo
1300	168.5	5.4	694	2	Q61P91_CABER	Q61p91	caenorhabdi
1301	168.5	5.4	728	2	Q6T546_LISMO	Q6t546	listeria mo
1302	168.5	5.4	744	2	Q8KTF6_LISMO	Q8ktf6	listeria mo
1303	168.5	5.4	791	2	Q2L8H6_LISMO	Q2l8h6	listeria mo
1304	168.5	5.4	800	2	Q4EQX8_LISMO	Q4eqx8	listeria mo
1305	168.5	5.4	907	1	LGR5_MOUSE	Q9zlp4	mus musculus
1306	168.5	5.4	1036	2	Q9FN37_ARATH	Q9fn37	arabidopsis
1307	168.5	5.4	1360	2	Q9ND11_DROME	Q9nd11	drosophila
1308	168.5	5.4	1724	2	Q4H4B6_BRARE	Q4h4b6	brachydanio
1309	168.5	5.4	3201	2	Q2QBE0_9ALPH	Q2qbe0	cercopithec
1310	168	5.4	351	2	Q65YW8_XENLA	Q65yw8	xenopus lae
1311	168	5.4	351	2	Q32N68_XENLA	Q32n68	xenopus lae
1312	168	5.4	402	2	Q72U35_LEPIC	Q72u35	leptospiira
1313	168	5.4	753	2	Q9NRE6_HUMAN	Q9nre6	homo sapien
1314	168	5.4	773	2	Q5NRE35_LISMO	Q5ne35	listeria mo
1315	168	5.4	951	1	LGRA_HUMAN	Q9bxt1	homo sapien
1316	168	5.4	977	2	Q8GVW0_ORYSA	Q8gvw0	oryza sativ
1317	168	5.4	1050	2	Q2GL4T3_CANFA	Q2gl4t3	canis fami
1318	167.5	5.3	147	2	Q9TT00_PIG	Q9tt00	sus scrofa
1319	167.5	5.3	171	2	Q2VHC1_PETMA	Q2vhc1	petromyzon
1320	167.5	5.3	185	2	Q2VGV4_PETMA	Q2vgv4	petromyzon
1321	167.5	5.3	351	1	KERA_MOUSE	Q35367	mus musculus
1322	167.5	5.3	360	1	PGS2_SHEEP	Q9ttc2	ovis aries
1323	167.5	5.3	378	2	Q72U36_LEPIC	Q72u36	leptospiira
1324	167.5	5.3	396	2	Q8C3D9_MOUSE	Q8c3d9	mus musculus
1325	167.5	5.3	422	1	OMD_BOVIN	Q77742	bos taurus
1326	167.5	5.3	694	2	Q4RYL2_TETNG	Q4ryl2	tetraodon n
1327	167.5	5.3	907	2	Q3V1L2_MOUSE	Q3vl12	mus musculus
1328	167.5	5.3	917	2	Q75GM9_ORYSA	Q75gm9	oryza sativ
1329	167.5	5.3	1174	2	Q7X537_ORYSA	Q7x537	oryza sativ
1330	167	5.3	168	2	Q2VGM8_PETMA	Q2vgm8	petromyzon
1331	167	5.3	262	2	Q2YE18_EPTST	Q2ye18	eptatretus
1332	167	5.3	537	2	Q6P2A4_RAT	Q6p2a4	rattus norv
1333	167	5.3	582	2	Q6AY15_RAT	Q6ay15	rattus norv
1334	167	5.3	633	2	Q8F3F6_LEPIN	Q8f3f6	leptospiira
1335	167	5.3	743	2	Q84CF7_LISMO	Q84cf7	listeria mo
1336	167	5.3	744	2	Q8KTF4_LISMO	Q8ktf4	listeria mo
1337	167	5.3	794	2	Q6YW99_ORYSA	Q6yw99	oryza sativ
1338	167	5.3	838	1	TLR4_CRIGR	Q9wv82	cricketulus
1339	167	5.3	886	2	Q469S7_METRA	Q469s7	methanosarc
1340	167	5.3	939	2	Q4SZU0_TETNG	Q4szu0	tetraodon n
1341	167	5.3	1112	2	Q41397_LYCPM	Q41397	lycopersico
1342	167	5.3	1112	2	Q41398_LYCPM	Q41398	lycopersico
1343	167	5.3	1112	2	Q4G2W2_LYCPM	Q4g2w2	lycopersico
1344	167	5.3	1263	2	Q4SID1_TETNG	Q4sid1	tetraodon n
1345	167	5.3	1845	2	Q5QNQ9_MOUSE	Q5qnq9	mus musculus

Q6e4d4	petromyzon	2	Q6E4D4_PETMA	163	5.3	1346	166.5
Q2vgj9	petromyzon	2	Q2VGJ9_PETMA	185	5.3	1347	166.5
Q3kq16	xenopus lae	2	Q3KQ16_XENLA	351	5.3	1348	166.5
Q3zbn5	bos taurus	2	Q3ZBN5_BOVIN	370	5.3	1349	166.5
Q5ne36	listeria mo	2	Q5NE36_LISMO	483	5.3	1350	166.5
Q9svw8	arabidopsis	2	Q9SVW8_ARATH	549	5.3	1351	166.5
Q5r423	pongo pygma	2	Q5R423_PONPY	582	5.3	1352	166.5
Q84cf6	listeria mo	2	Q84CF6_LISMO	739	5.3	1353	166.5
Q8kff9	listeria mo	2	Q8KTF9_LISMO	741	5.3	1354	166.5
Q8kff9	listeria mo	2	Q8KTF9_LISMO	741	5.3	1355	166.5
Q95rv9	drosophila	2	Q95RV9_DROME	743	5.3	1356	166.5
Q8kft2	listeria mo	2	Q8KTF2_LISMO	743	5.3	1357	166.5
Q8khn1	listeria mo	2	Q8KHN1_LISMO	744	5.3	1358	166.5
Q8k188	listeria mo	2	Q8K188_LISMO	744	5.3	1359	166.5
Q8kff1	listeria mo	2	Q8KTF1_LISMO	744	5.3	1360	166.5
Q8kff5	listeria mo	2	Q8KTF5_LISMO	744	5.3	1361	166.5
Q8kff8	listeria mo	2	Q8KTF8_LISMO	744	5.3	1362	166.5
Q8kff3	listeria mo	2	Q8KTF3_LISMO	746	5.3	1363	166.5
Q5ne37	listeria mo	2	Q5NE37_LISMO	792	5.3	1364	166.5
Q2l8g9	listeria mo	2	Q2L8G9_LISMO	794	5.3	1365	166.5
Q2l8h1	listeria mo	2	Q2L8H1_LISMO	794	5.3	1366	166.5
Q2l8h2	listeria mo	2	Q2L8H2_LISMO	794	5.3	1367	166.5
Q2l8h3	listeria mo	2	Q2L8H3_LISMO	794	5.3	1368	166.5
Q2l8h4	listeria mo	2	Q2L8H4_LISMO	794	5.3	1369	166.5
Q2l8h5	listeria mo	2	Q2L8H5_LISMO	794	5.3	1370	166.5
Q2l8h7	listeria mo	2	Q2L8H7_LISMO	794	5.3	1371	166.5
Q4ej83	listeria mo	2	Q4EJ83_LISMO	797	5.3	1372	166.5
Q723x6	listeria mo	1	INLA_LISMF	800	5.3	1373	166.5
P25146	listeria mo	1	INLA_LISMO	800	5.3	1374	166.5
Q45gd5	listeria mo	2	Q45GD5_LISMO	800	5.3	1375	166.5
Q45gd6	listeria mo	2	Q45GD6_LISMO	800	5.3	1376	166.5
Q95vi6	asterina pe	2	Q95VI6_ASTPE	1012	5.3	1377	166.5
Q65x29	oryza sativ	2	Q652D9_ORYSA	1115	5.3	1378	166.5
Q60p92	caenorhabdi	2	Q60PY2_CABER	1215	5.3	1379	166.5
Q7qnp7	anopheles g	2	Q7QHP7_ANOGA	1270	5.3	1380	166.5
Q95vi7	asterina pe	2	Q95VI7_ASTPE	1280	5.3	1381	166.5
Q6x248	bovine heip	2	Q6X248_9ALPH	3204	5.3	1382	166.5
Q6ef8	petromyzon	2	Q6E8F8_PETMA	163	5.3	1383	166
Q2vbk9	petromyzon	2	Q2VGK9_PETMA	170	5.3	1384	166
Q2vbk1	petromyzon	2	Q2VGK1_PETMA	192	5.3	1385	166
Q4kp01	lampetra ap	2	Q4KP01_LAMAP	245	5.3	1386	166
Q3utg8	mus musculus	2	Q3UTG8_MOUSE	393	5.3	1387	166
Q72tc3	leptospiira	2	Q72TC3_LEPIC	426	5.3	1388	166
Q4sse3	tetraodon n	2	Q4SSE3_TETNG	768	5.3	1389	166
Q6p90	rattus norv	2	Q6P90_RAT	806	5.3	1390	166
Q9x05	rattus norv	2	Q9X05_RAT	835	5.3	1391	166
Q51m3	sus scrofa	1	TLR4_RAT	1030	5.3	1392	166
Q865r8	sus scrofa	1	TLR9_PIG	1030	5.3	1393	166
Q7g768	oryza sativ	2	Q7G768_ORYSA	1110	5.3	1394	166
Q9n523	caenorhabdi	2	Q9N523_CABEL	1221	5.3	1395	166
Q4pdw0	ustilago ma	2	Q4PDM0_USTMA	2139	5.3	1396	166
Q2vgk0	petromyzon	2	Q2VGK0_PETMA	161	5.3	1397	165.5
Q2vgh0	petromyzon	2	Q2VGH0_PETMA	169	5.3	1398	165.5
Q2vgu2	petromyzon	2	Q2VGU2_PETMA	195	5.3	1399	165.5
Q5rhe5	brachydanio	2	Q5RHE5_BRARE	327	5.3	1400	165.5
P21793	bos taurus	2	PGS2_BOVIN	360	5.3	1401	165.5
Q29393	canis fami	1	PGS2_CANFA	360	5.3	1402	165.5
Q3mhn1	bos taurus	2	Q3MHN1_BOVIN	360	5.3	1403	165.5
Q7xj53	arabidopsis	2	Q7XJ53_ARATH	526	5.3	1404	165.5
Q5h716	fugu rubrip	2	Q5H716_FUGRU	641	5.3	1405	165.5
Q31273	sparus aura	2	Q3I273_SPAU	1005	5.3	1406	165.5
Q31274	sparus aura	2	Q3I274_SPAU	1063	5.3	1407	165.5
Q59h95	homo sapien	2	Q59H95_HUMAN	1101	5.3	1408	165.5
Q24020	drosophila	2	FLII_DROME	1256	5.3	1409	165.5
Q13045	homo sapien	1	FLII_HUMAN	1269	5.3	1410	165.5
Q5r4g9	pongo pygma	2	Q5R4G9_PONPY	1269	5.3	1411	165.5
Q2vh02	petromyzon	2	Q2VH02_PETMA	196	5.3	1412	165
Q4rx02	tetraodon n	2	Q4RX02_TETNG	283	5.3	1413	165
Q5r6f8	pongo pygma	2	Q5R6F8_PONPY	436	5.3	1414	165
Q7ryp2	neuropora	2	Q7RYP2_NEUCR	902	5.3	1415	165
Q32nj0	xenopus lae	2	Q32NJ0_XENLA	955	5.3	1416	165
Q9c637	arabidopsis	2	Q9C637_ORYSA	994	5.3	1417	165
Q7xs12	oryza sativ	2	Q7XS12_ORYSA	1135	5.3	1418	165



1419	165	5.3	1154	2	Q7QHH4	ANOGA	Q7qhh4	anopheles g	1492	162.5	5.2	452	2	Q8F118	LEPIN	Q8f118	leptospira
1420	164.5	5.2	171	2	Q2VH95	PETMA	Q2vhu95	petromyzon	1493	162.5	5.2	494	2	Q9VEK6	DROME	Q9vek6	drosofila
1421	164.5	5.2	185	2	Q2VGH7	PETMA	Q2vgh7	petromyzon	1494	162.5	5.2	527	2	Q86PB5	DROME	Q86pb5	drosofila
1422	164.5	5.2	235	2	Q4G1H9	EPTST	Q4gh9	eptaretus	1495	162.5	5.2	641	2	Q8QMO0	DROME	Q8qmo0	drosofila
1423	164.5	5.2	468	2	Q44V99	9BURK	Q44v99	burholderi	1496	162.5	5.2	700	2	Q4R6H5	MACFA	Q4r6h5	macaca fasc
1424	164.5	5.2	468	2	Q4LVE2	9BURK	Q4lve2	burholderi	1497	162.5	5.2	1045	2	Q5H717	FUGRU	Q5h717	fugu rubrip
1425	164.5	5.2	582	1	SHOC22	HUMAN	Shoc22	homo sapien	1498	162	5.2	168	2	Q2VGH2	PETMA	Q2vgh2	petromyzon
1426	164.5	5.2	582	2	Q5VZS9	HUMAN	Q5vzs9	homo sapien	1499	162	5.2	168	2	Q2VH77	PETMA	Q2vh77	petromyzon
1427	164.5	5.2	582	2	Q5RAV5	PONPY	Q5rav5	pongo pygma	1500	162	5.2	192	2	Q2VH10	PETMA	Q2vh10	petromyzon
1428	164.5	5.2	611	2	Q2RBL3	ORYSA	Q2rbl3	oryza sativ									
1429	164.5	5.2	734	2	Q5R7N1	PONPY	Q5r7n1	pongo pygma									
1430	164.5	5.2	805	2	Q658W7	HUMAN	Q658w7	homo sapien									
1431	164.5	5.2	819	2	Q659A9	HUMAN	Q659a9	homo sapien									
1432	164.5	5.2	858	1	LRC9D	HUMAN	Q7llw4	homo sapien									
1433	164.5	5.2	858	1	Q2XXU4	DROYA	Q2xxu4	drosofila									
1434	164.5	5.2	1421	2	Q2XXU5	DROYA	Q2xxu5	drosofila									
1435	164	5.2	1426	2	LRRX3	MOUSE	P59034	mus musculus									
1436	164	5.2	257	1	LRRX3	MOUSE	P59034	mus musculus									
1437	164	5.2	257	2	Q543Z4	MOUSE	Q543z4	mus musculus									
1438	164	5.2	446	2	Q8F213	LEPIN	Q8f213	leptospira									
1439	164	5.2	441	2	Q399Q6	BURS3	Q399q6	burholderi									
1440	164	5.2	515	2	Q60MT7	CAEBR	Q60mt7	caenorhabdi									
1441	164	5.2	559	2	Q60UG7	CAEBR	Q60ug7	caenorhabdi									
1442	164	5.2	570	2	Q8L3T8	ORYSA	Q8l3t8	oryza sativ									
1443	164	5.2	611	2	Q7T062	MOUSE	Q7t062	mus musculus									
1444	164	5.2	636	1	SLIK1	HUMAN	Q96px8	homo sapien									
1445	164	5.2	636	1	SLIK1	MOUSE	Q810c1	mus musculus									
1446	164	5.2	696	1	SLIK1	PONPY	Q5rac4	pongo pygma									
1447	164	5.2	760	2	Q69Z70	MOUSE	Q69z70	mus musculus									
1448	164	5.2	805	2	Q7QFF0	ANOGA	Q7qff0	anopheles g									
1449	164	5.2	807	2	Q2M124	DROPS	Q2m124	drosofila									
1450	164	5.2	828	1	LGR6	HUMAN	Q9hbx8	homo sapien									
1451	164	5.2	833	2	Q7QI8	ANOGA	Q7qi8	anopheles g									
1452	164	5.2	839	2	Q8MTQ2	RABIT	Q8mtq2	oryctolagus									
1453	164	5.2	870	2	Q6PCD4	HUMAN	Q6pcd4	homo sapien									
1454	164	5.2	904	1	TLR3	HUMAN	Q15455	homo sapien									
1455	164	5.2	904	2	Q4VAL2	HUMAN	Q4val2	homo sapien									
1456	164	5.2	904	2	Q504W0	HUMAN	Q504w0	homo sapien									
1457	164	5.2	1032	2	Q865B9	CANFA	Q865b9	canis famil									
1458	164	5.2	1395	2	Q7SC01	NEUCR	Q7sc01	neurospora									
1459	164	5.2	1913	2	Q5SVA2	HUMAN	Q5sva2	homo sapien									
1460	164	5.2	2045	1	AGRN	HUMAN	Q00468	homo sapien									
1461	163.5	5.2	163	2	Q6FE1	HUMAN	Q6fe1	homo sapien									
1462	163.5	5.2	166	2	Q6E4E0	PETMA	Q6e4e0	petromyzon									
1463	163.5	5.2	180	2	Q6E4H7	PETMA	Q6e4h7	petromyzon									
1464	163.5	5.2	185	2	Q2VGF3	PETMA	Q2vgf3	petromyzon									
1465	163.5	5.2	195	2	Q2VGX2	PETMA	Q2vgx2	petromyzon									
1466	163.5	5.2	362	2	Q502F2	ERARE	Q502f2	brachydanio									
1467	163.5	5.2	370	2	Q9DB04	ORENI	Q9db04	oreochromis									
1468	163.5	5.2	582	2	Q5RSR1	PONPY	Q5rsr1	pongo pygma									
1469	163.5	5.2	671	2	Q53GZ4	HUMAN	Q53gz4	homo sapien									
1470	163.5	5.2	786	2	Q48809	ARATH	Q48809	arabidopsis									
1471	163	5.2	168	2	Q2VH67	PETMA	Q2vh67	petromyzon									
1472	163	5.2	170	2	Q2VH86	PETMA	Q2vh86	petromyzon									
1473	163	5.2	172	2	Q2VGT3	PETMA	Q2vgt3	petromyzon									
1474	163	5.2	192	2	Q2VGE0	PETMA	Q2vge0	petromyzon									
1475	163	5.2	194	2	Q2VGV9	PETMA	Q2vgv9	petromyzon									
1476	163	5.2	359	2	Q9DS03	ORENI	Q9de03	oreochromis									
1477	163	5.2	452	2	Q4RB66	TETNG	Q4rb66	tetraodon n									
1478	163	5.2	501	2	Q6ZH85	ORYSA	Q6zh85	oryza sativ									
1479	163	5.2	524	2	Q8R378	MOUSE	Q8r378	mus musculus									
1480	163	5.2	582	1	SHOC2	MOUSE	Q88520	mus musculus									
1481	163	5.2	582	2	Q3UJH6	MOUSE	Q3ujh6	mus musculus									
1482	163	5.2	929	2	Q6P9N3	MOUSE	Q6p9n3	mus musculus									
1483	163	5.2	933	2	Q9BDU5	STRPU	Q9bd5	strongyloce									
1484	163	5.2	961	2	Q76CT7	PAROL	Q76ct7	paralichthy									
1485	163	5.2	961	2	Q76CT9	PAROL	Q76ct9	paralichthy									
1486	163	5.2	1221	2	Q9BIW9	CAEBL	Q9biw9	caenorhabdi									
1487	163	5.2	1612	1	LAP4	MOUSE	Q80u72	mus musculus									
1488	162.5	5.2	161	2	Q2VHE8	PETMA	Q2vhe8	petromyzon									
1489	162.5	5.2	192	2	Q2VGT1	PETMA	Q2vgt1	petromyzon									
1490	162.5	5.2	283	2	Q9V428	DROME	Q9v428	drosofila									
1491	162.5	5.2	375	2	Q5XIH1	RAT	Q5xih1	rattus norv									

## ALIGNMENTS

## RESULT 1

Q6UKL5 HUMAN  
 ID Q6UKL5 HUMAN PRELIMINARY; PRT; 598 AA.  
 AC Q6UKL5;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE CSRV314.  
 GN ORFNames=UNQ314;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
 Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 Eaton D., Foster J.S., Grimaldi C., Gu O., Hass P.E., Heldens S.,  
 Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,  
 Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
 Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,  
 Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
 Wood W.I., Godowski P.J., Gray A.M.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 effort to identify novel human secreted and transmembrane proteins: a  
 bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
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EMBL: AY358298; AAQ88665.1; -; mRNA.

InterPro: IPR006210; EGF.

InterPro: IPR000742; EGF\_3.

InterPro: IPR006209; EGF\_like.

InterPro: IPR013032; EGF\_like\_reg.

InterPro: IPR003961; FN\_III.

InterPro: IPR001611; LRR.

InterPro: IPR000483; LRR\_C.

InterPro: IPR000372; LRR\_Cys\_N.

InterPro: IPR003591; LRR\_typ.

Pfam: PF00008; EGF\_1.

Pfam: PF00041; fn3\_1.

Pfam: PF00560; LRR\_1; 3.

Pfam: PF01463; LRRCT; 1.

Pfam: PF01462; LRRNT; 1.

PRINTS: PR00019; LEURICRPT.

SMART: SM00181; EGF; 1.

SMART: SM00082; LRRCT; 1.

SMART: SM00013; LRRNT; 1.

PROSITE: PS00022; EGF\_1; 1.

PROSITE: PS01186; EGF\_2; 1.

PROSITE: PS50026; EGF\_3; 1.

PROSITE: PS50853; FN3; 1.

SEQUENCE 598 AA; 63030 MW; C596CEBE963AA86C CRC64;



Query Match 100.0%; Score 3135; DB 2; Length 598;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-171;  
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QY 61 ENGITMLDASSFAGLPGQLDLSQNOIASRLPRLLLDLSHNSLLALEPGILDTANVE 120  
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QY 181 RPEDLAGLAQBELDVSNSLSQALPGDLSGLFRLRLAALAAARNPFCVPLSFWGFWVRE 240  
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QY 241 SHVTLASPEPTRCHFPKNAKRLLELDYADFQCPATTTATVTPTRPVVREPTALSSSL 300  
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QY 301 APTWLSPTAPATAPSPPTAPTVGPVPOQPCPSTCLNGCTCHLGRHLACLCPEG 360  
 DB 301 APTWLSPTAPATAPSPPTAPTVGPVPOQPCPSTCLNGCTCHLGRHLACLCPEG 360

QY 361 FTGLYCESQMGCTRSPTPTVTPRPSRLTLGIEPVSPTRSLRVLQRYLQGSVQLRSLR 420  
 DB 361 FTGLYCESQMGCTRSPTPTVTPRPSRLTLGIEPVSPTRSLRVLQRYLQGSVQLRSLR 420

QY 421 LTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATYSVCMPLGPGVPEGEACGEAHT 480  
 DB 421 LTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATYSVCMPLGPGVPEGEACGEAHT 480

QY 481 PPAVSHNHAPVTOAREGNLPLLTAPALAAVLLAALAAVGAAYCVRGRAMAAAQDKGV 540  
 DB 481 PPAVSHNHAPVTOAREGNLPLLTAPALAAVLLAALAAVGAAYCVRGRAMAAAQDKGV 540

QY 541 GPGAGPLELGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPGLQSLPHAKPYI 598  
 DB 541 GPGAGPLELGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPGLQSLPHAKPYI 598

RESULT 2  
 ID Q6UXL4 HUMAN PRELIMINARY; PRT; 673 AA.  
 AC Q6UXL4;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 16.  
 DE CSRV314 (slit-like 2).  
 GN Name=SLITL2; ORFNames=UNQ114;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
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 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,  
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
 RA Wood W.I., Godowski P.J., Gray A.M.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 effort to identify novel human secreted and transmembrane proteins: a

bioinformatics assessment.";  
 Genome Res. 13:2265-2270(2003).  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Hulyk S.W.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 RG NIH MGC Project;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL; AY358299; AAQ88666.1; -; mRNA.  
 DR EMBL; BC068575; AAH68575.1; -; mRNA.  
 DR Ensembl; ENSG00000168140; Homo sapiens.  
 DR InterPro; IPR006210; EGF.  
 DR InterPro; IPR000742; EGF\_3.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR013032; EGF\_like\_reg.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_C.  
 DR InterPro; IPR000372; LRR\_cys\_N.  
 DR InterPro; IPR003885; LRR\_cyst.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00041; fn3; 1.  
 DR Pfam; PF00560; LRR\_1; 6.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR Pfam; PF01462; LRRNT; 1.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00369; LRR\_TYP; 2.  
 DR SMART; SM00082; LRRCT; 1.  
 DR SMART; SM00013; LRRNT; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS50853; FN3; 1.  
 DR SQUENCE 673 AA; 71655 MW; 4CFA391231D4BF8 CRC64;

Query Match 98.4%; Score 3083.5; DB 2; Length 673;  
 Best Local Similarity 88.7%; Pred. No. 1.2e-168;  
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QY 61 ENGITMLDASSFAGLPGQLDLSQNOIASRLPRLLLDLSHNSLLALEPGILDTANVE 120  
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QY 121 ALRLAGLGLQOLDEGLFSRLNLHDLVDSDNQLERVPVIRGLGTRLRLAGNTRIAOL 180  
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QY 181 RPEDLAGLAQBELDVSNSLSQALPGDLSGLFRLRLAALAAARNPFCVPLSFWGFWVRE 240  
 DB 181 RPEDLAGLAQBELDVSNSLSQALPGDLSGLFRLRLAALAAARNPFCVPLSFWGFWVRE 240

QY 241 SHVTLASPEPTRCHFPKNAKRLLELDYADFQCPATTTATVTPTRPVVREPTALSSSL 300  
 DB 241 SHVTLASPEPTRCHFPKNAKRLLELDYADFQCPATTTATVTPTRPVVREPTALSSSL 300

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 DB 301 APTWLSPTAPATAPSPPTAPTVGPVPOQPCPSTCLNGCTCHLGRHLACLCPEG 360

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 DB 361 FTGLYCESQMGCTRSPTPTVTPRPSRLTLGIEPVSPTRSLRVLQRYLQGSVQLRSLR 420

QY 421 LTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATYSVCMPLGPGVPEGEACGEAHT 480  
 DB 421 LTYRNLSGDPKRLVTLRLPASLAETVTLQRPNATYSVCMPLGPGVPEGEACGEAHT 480

QY 481 PPAVSHNHAPVTOAREGNLPLLTAPALAAVLLAALAAVGAAYCVRGRAMAAAQDKGV 540  
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QY 541 GPGAGPLELGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPGLQSLPHAKPYI 598  
 DB 541 GPGAGPLELGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPGLQSLPHAKPYI 598



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Qy 91 -----LRLPRLLLLDLSHNS 105
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Db 181 LLALEPGILDTANVEALRLAGLQGLDGLFSRLNLHDLVDNSQLERVPPVIRGLRG 240
Qy 166 LTRLRAGNTRIAQLRPEDLAGLAAQLDGLVNSLSQALPGDLSGLFPRLRLAARNP 225
Db 241 LTRLRAGNTRIAQLRPEDLAGLAAQLDGLVNSLSQALPGDLSGLFPRLRLAARNP 300
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Db 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFFPKNAGRLLELDYADFGCPATTTATVPT 360
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Db 481 QRYLOGSSVQLRSRLTYRNLGGPKRLVTLRLPASLAETVTQLRPNATYVSCVMPGLP 540
Qy 466 GRVPEGEACGEAHTPPAVSHNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVR 525
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Qy 526 RGRWAAAAQDKGVGPGAGLEBKVPLPBGKATEGGGEALPSGSECEVPLMGPG 585
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Qy 586 PGLQSPHLHAKPYI 598
Db 661 PGLQSPHLHAKPYI 673

RESULT 3
QEMK4 HUMAN
ID Q6EMK4.HUMAN PRELIMINARY; PRT; 673 AA.
AC Q6EMK4.
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Vasorin.
GN Name=SLIT2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15247411; DOI=10.1073/pnas.0404117101;
RA Ikeda Y., Imai Y., Kumagai H., Nohara T., Morikawa Y., Hiseoka T.,
RA Manabe I., Maemura K., Nakaoka T., Imamura T., Miyazono K., Komuro I.,
RA Nagai R., Kitamura T.;
RT "Vasorin, a transforming growth factor [beta]-binding protein
RT expressed in vascular smooth muscle cells, modulates the arterial
RT response to injury in vivo."
RL Proc. Natl. Acad. Sci. U.S.A. 101:10732-10737(2004).
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DB EMBL; AY166584; AAO27704.1; -; mRNA.
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DR Ensembl; ENSG00000168140; Homo sapiens.
DR HGNC; HGNC:18517; SLIT2.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF 3.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR013032; EGF-like_reg.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR C.
DR InterPro; IPR000372; LRR cyst.
DR InterPro; IPR003885; LRR cyst.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; FN3; 1.
DR Pfam; PF00560; LRR_1; 6.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 1.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
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DR PROSITE; PS50853; FN3; 1.
DR SEQUENCE 673 AA; 71713 MW; 891E149652DEA286 CRC64;

Query Match 98.2%; Score 3078.5; DB 2; Length 673;
Best Local Similarity 88.6%; Pred No. 2.4e-168;
Matches 596; Conservative 0; Mismatches 2; Indels 75; Gaps 1;

Qy 1 MCSRVPLLLPLLLLLALGPGVQCGSPGCGSQCPQVFTARQGTTPRDPVPTVGLYVF 60
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Db 61 ENGITMLDAGSFAGLQGLDLSQNIAS ----- 120
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Db 121 RGLRLRLYLGNRIHQPCAFDTLDRLLLEKLQDNELRALPPLRLPRLLLLDLSHNS 180
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Db 181 LLALEPGILDTANVEALRLAGLQGLDGLFSRLNLHDLVDNSQLERVPPVIRGLRG 240
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Db 241 LTRLRAGNTRIAQLRPEDLAGLAAQLDGLVNSLSQALPGDLSGLFPRLRLAARNP 300
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Qy 286 TRPVVREPTALSSSLAPTWSLPTAPATEAPSPPTAPPTVGVPOQDCPPSTCLNGGTC 345
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RESULT 4
Q96CX1 HUMAN
ID Q96CX1_HUMAN PRELIMINARY; PRT; 601 AA.
AC Q96CX1;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE SLTL2 protein (Fragment).
GN Name=SLTL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
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RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Hopkins R.F., Jordan H., Moore H., Max S.T., Wang J., Hsieh F.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC HMBL; BC013767; AAH13767.1; -; mRNA.
DR HSP; Q9BZR6; 1P8T.
DR Ensembl; ENSG00000168140; Homo sapiens.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR000742; EGF_3.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR013032; EGF_like_reg.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR004483; LRR_C.
DR InterPro; IPR003885; LRR_cyst.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00560; LRR_1; 6.
DR Pfam; PF01463; LRRCT; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00181; EGF; 1.
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DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00082; LRRCT; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS0853; FN3; 1.
KW EGF-like domain; Leucine-rich repeat.
FT NON TER 1
SQ SEQUENCE 601 AA; 64179 MW; 4964077778D9ABD2 CRC64;

Query Match 86.0%; Score 2697.5; DB 2; Length 601;
Best Local Similarity 87.4%; Pred. No. 1.5e-146;
Matches 525; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

QY 73 AGLPGLQLLDLSQNIAS----- 90
Db 1 AGLPGLQLLDLSQNIASLPSGVFQPLANLSNLDLTANRLHEITNETPRGRRLRLRYLG 60
QY 91 -----LRLPRLLLDLSHNSILALEPGILDTA 117
Db 61 KNIRHIQPGAFDTLRLLELKLQDNELRALPPLRLPRLLLDLSHNSILALEPGILDTA 120
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Db 121 NVEALRLAGLQQLDEGLFSRLRNLDLDVSDNQLRVPVIRGLRGLTRLRAGNTRI 180
QY 178 AOLRPEDLAGLAALQELDVSNLSLOALPGDLSGLFPRLLRLAAARNPNCVPLSWFGPW 237
Db 181 AOLRPEDLAGLAALQELDVSNLSLOALPGDLSGLFPRLLRLAAARNPNCVPLSWFGPW 240
QY 238 VRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTTATVTPTRPVVREPTALS 297
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QY 598 1 598
Db 601 1 601

RESULT 5
Q8BJJ0 MOUSE
ID Q8BJJ0_MOUSE PRELIMINARY; PRT; 673 AA.
AC Q8BJJ0;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE 9 days embryo whole body cDNA, RIKEN full-length enriched library,
DE clone:D03006D07 product.hypothetical prokaryotic membrane lipoprotein
DE lipid attachment site/cysteine-rich flanking region, N-
DE terminal/Leucine-rich repeat/EGF-like domain/Leucine-rich repeat.
DE typical subtype/Leucine-rich repeat, outliers/cysteine-rich flanking
DE region, C-terminal/Leucine-rich region/Fibronectin type III domain
DE containing protein, full insert sequence.
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GN Name-Slit12;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
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 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Methods Enzymol. 303:19-44(1999).  
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 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
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 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
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 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
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 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
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 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,  
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 RA Petkovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
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 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,  
 RA Tammoja K., Tan S.B., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
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 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
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 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).  
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 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566(2005).  
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 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
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 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
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 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
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 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [5]  
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 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
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 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
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 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
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 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
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 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
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 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
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 RL Genome Res. 10:1757-1771(2000).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE.







- RA Director MGC Project;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
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RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Methods Enzymol. 303:19-44(1999).  
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RX PubMed=16141072; DOI=10.1126/science.1112014;  
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RT "The transcriptional landscape of the mammalian genome.";  
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RG RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566(2005).  
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RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi H., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Clothia C., Corbani L.E., Cousins S., Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Tesdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [8]  
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RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;  
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RL Nature 409:685-690(2001).  
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RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
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OC Muroidea; Muridae; Murinae; Mus.  
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RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RT Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning.";  
RL Methods Enzymol. 303:19-44(1999).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX PubMed=16141073; DOI=10.1126/science.11112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilmink L.G., Adinolf V., Allen J.E., Ambesi-Impombato A., Apeztegui R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., Di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Humaneck I.L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Mottagui-Tabar S., Mulder N., Nakano N., Nakaochi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Read J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno K., Nakano N., Nimomiya N., Nishio T., Okada M., Olesch A., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Wataniki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome.";  
RL Science 309:1559-1563(2005).  
[3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RG RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566(2005).  
[4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Whole body;  
RX MEDLINE=22354683; PubMed=12456851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Glisi C., Godzik A., Gough J., Graimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,







Db 367 REPTLSTSQAPTWPRLTETFTQASTVLTAPPTWMPAPQPOQCPASICLNGSGSCELGAR 426  
QY 351 HHLACLCPGFTGLYCESQMGQTRSPPTVTPRPRSLTLGIEPVSPSLRVGLQRYLQ 410  
Db 427 HHWECLCPGFTGLYCESPVEQGMKSSIPDTPRPPPLPLSLIEPVSPSLRVGLQRYLQ 486  
QY 411 GSSVQLSRLLTYRNLSGDPKRLVTLRLPASLAAYVTQLRPNATYVSCVMPILGPRVPE 470  
Db 487 GNTVQLSRLLTYRNLSGDPKRLVTLRLPASLAAYVTQLRPNATYVSCVMPILGAGRTPE 546  
QY 471 GEEACGEAHTPPAVHNSHAPVTQAREGNLPLLIAPALAAVLLAAVGAACVVRGRAM 530  
Db 547 GEEACGEAHTPPAVHNSHAPVTQAREGNLPLLIAPALAAVLLAAVGAACVVRARA- 605  
QY 531 AAAAQDKGVGPGAGLEGVKVPLEPGPKATEGGEGALPGSGCEVPLMGPPGGLQS 590  
Db 606 TSAQDKGVGPGTGPLEGVKAPLEPGSKATEGGEGALSGGCEVPLMGVPGPSLQG 665  
QY 591 PLHAKPYI 598  
Db 666 VLPARKYI 673

RESULT 8

Q6DF55\_XENTR PRELIMINARY; PRT; 661 AA.  
AC Q6DF55;  
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.  
DT 16-AUG-2004, sequence version 1.  
DT 07-FEB-2006, entry version 12.  
DE MGC8956 protein.  
GN Name=MGC8956;  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus; Silurana.  
OX NCBI\_TaxID=8364;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Whole body;  
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Whole body;  
RC Klein S., Gerhart D.S.;  
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; BC076888; AAH76888.1; -, mRNA.  
DR InterPro; IPR006210; EGF.

DR InterPro; IPR00742; EGF 3.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR013032; EGF\_like\_reg.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR004883; LRR C.  
DR InterPro; IPR003885; LRR cyst.  
DR InterPro; IPR003591; LRR\_typ.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00560; LRR\_1; 8.  
DR Pfam; PF01463; LRRCT; 1.  
DR PRINTS; PRO0019; LEURICHRPT.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00369; LRR\_TYP; 5.  
DR SMART; SM00082; LRRCT; 1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS0026; EGF 3; 1.  
SQ SEQUENCE 661 AA; 71958 MW; A0AC47946BE8DBEA CRC64;  
  
Query Match 38.7%; Score 1213.5; DB 2; Length 661;  
Best Local Similarity 41.3%; Pred. No. 2.3e-61;  
Matches 282; Conservative 88; Mismatches 158; Indels 155; Gaps 20;  
  
QY 8 LLPLLLLLALGPGV--QGCPGCGSQPQTCTARQGTTPVRDVPDPTVGLYVFNENGIT 65  
Db 4 LLVWILLATAQOMITEGCPAGCQCNTPTQVFLARKNSNFRSPVPDPTLVLYVFNENGIS 63  
QY 66 MLDASFPAGLPGLQLLDLSQNIASL----- 91  
Db 64 STEESSFGLNGHLHLLDLSHNSLPGVGFVRNLANLSNLDLTSNQLTISADTFOGLSR 123  
QY 92 -----RLPLLLLDLSHNSLALAE 110  
Db 124 LERLYLNGNRIRSIHPEAFKGIESLELKLNNQLVTPPAFLPHLLLDLSNALPVIQ 183  
QY 111 PGILDTANVEALRLAGLQQLDEGLFSRLRLHLDVSDNQLERVPVIRGLRGLTRLR 170  
Db 184 QGVFNAGNIESRLAGLGLKEVPEELLGKLNHLDLSDNQLDKVPP--GLHGLTKLN 240  
QY 171 LAGNTRIAQLRPEDLAGLAALQELDVSNLSQALPGDLSGLPRLRLAAARNPFCVCP 230  
Db 241 IAGNVGFSQIQVDDLSNLPAQLQELDSLQTLPGKLFPSKRLRAVSLAQNFNCVCS 300  
QY 231 LSWFGPWRESHVTLASPEETECHPPKNAGRLLLELDYADGCPATTTTATVPTTRPVV 290  
Db 301 LGWLSEWFRVSGVLLRPDETRCHFPKNAGKTLRLDRDSEYGCPC-PTTIQMPSTWPP- 358  
QY 291 REPTALSSSLAPTWLSPTAP--ATEAPSPSTAPPTVGPVPOQD-----CP 335  
Db 359 -----STTGP-----PTTKHLQTEAPTASTTTTIPHQBQEDTQPPDFEDTLCP 408  
QY 336 PFTCLNGGTCHLGRHHLACLPEGFTGLYCSQMGQTRPSPTVTPRPPRSL---TLG 392  
Db 409 PQTCLNGGSCHLDPQTQLECECPGPGQTYCET-----GPVTPAVVTEMYIEQVK 458  
QY 393 IEPVSTSLRVGLORYLQSSVQLRSRLTYRNLSPDKELVTLRLPASLAAYVTQLRP 452  
Db 459 IIEVTVSSIRVDLQSYSONKE-KLRAIRLTVRNLYGADRREMIYKLPPTLPEYTVRALSS 517  
QY 453 NATYSCVVMPLGPRVPEGEACGEAHT---PPAVHNSHAP-VTOAREGNLPLLIAPALA 508  
Db 518 NSSYVWCLGSQEGG-PE-EDLCTETHLGEPP---KHSPQVTSQEGNLTVLVPAVA 571  
QY 509 AVLLAALAAVGAAYCVRRGRAMAAAAQDKGVGPGAGLEGVKVPLEPGPKATEGGEG 568  
Db 572 AGILLS-AAVAAAACVARRR-----KKGHGSVEDGGPLEMDGVK-----KGLDGKGE 617  
QY 569 AL-----PSGSECEVPLM 581  
Db 618 VKKLSBDPTGPEKTGAESSEPLM 640  
  
RESULT 9



Q3MKW9\_BRARE  
ID Q3MKW9\_BRARE PRELIMINARY; PRT; 688 AA.  
AC Q3MKW9;  
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.  
DT 25-OCT-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE Slit-like 2 protein.  
GN Names:slit2;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=AB;  
RX PubMed=1612671; DOI=10.1016/j.bbrc.2005.08.071;  
RA Chen L., Yao J.H., Zhang S.H., Wang L., Song H.D., Xue J.L.;  
RT "Slit-like 2, a novel zebrafish slit homologue that might involve in  
zebrafish central neural and vascular morphogenesis.";  
RL Biochem. Biophys. Res. Commun. 336:364-371(2005).  
CC  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
EMBL; AY838878; AA057297.1; -; mRNA.  
ZFIN; ZDB-GENE-050522-43; slitl2.  
DR InterPro; IPR000742; EGF\_3.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR013032; EGF like\_reg.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR000119; Hist\_DNA\_bd\_bac.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000483; LRR\_C.  
DR InterPro; IPR000372; LRR\_cys\_N.  
DR InterPro; IPR003885; LRR\_cysT.  
DR InterPro; IPR003591; LRR\_tyr.  
DR Pfam; PF00008; EGF\_1.  
DR Pfam; PF00560; LRR\_1; 7.  
DR Pfam; PF01462; LRRNT; 1.  
DR PRINTS; PR00019; LEURICHRPT.  
DR SMART; SM00369; LRR\_TYP; 2.  
DR SMART; SM00082; LRRCT; 1; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS50026; EGF\_3; 1.  
DR PROSITE; PS50853; FN3; 1.  
DR PROSITE; PS00045; HISTONE LIKE; UNKNOWN\_1.  
SQ SEQUENCE 688 AA; 75284 Mw; 4E197B063AF3608C CRC64;  
Query Match 31.0%; Score 972.5; DB 2; Length 688;  
Best Local Similarity 36.3%; Pred. No. 1.6e-47;  
Matches 239; Conservative 77; Mismatches 222; Indels 121; Gaps 15;  
QY 6 PLLPLLLALLGPGVQCGSPGCGCQSQPQTVFCTARQGTTPRDVDPDTVGLVFNENGIT 65  
Db 6 PLSHLILLQLCCLSRCHDCTCLPSNNIFCVQRNLNLYMPRGLPSTGKQLYVFQNKIN 65  
QY 66 MLDASSFAGLPGIQLLDLSONQIA----- 89  
Db 66 ILQQQDFVELGELEMLDLSONSLSEIPDGVFSPLSLHNLDLSSNITHSKDSFGLVNLN 125  
QY 90 -----SLRLPRLLLDLSHNSLLALE 110  
Db 126 LERLYLSNIIQNIHPAAFEGLNLELKLQGNQISVLPAQLQLPRLHLDLSYNSIPPLV 185  
QY 111 PGLTDANVEALRAGLGLOOLDEGLFSLRLNHLHDLDVSDNQLRVPVIRGLRGLTRLR 170  
Db 186 AQDLQTPHLESKIAGLGLTSLDEELGLSVNLHVLDSVQNLVDIQPTLKSNGGLRLNLN 245  
QY 171 LAGNTRIAQLRPEDLAGLAALQDLDSGLFSLRLRLAAARNPFCVCP 230  
Db 246 LTGNP-LGSLKHEDFQNLVNLLELDLSNLNLQGFPEGFNLFPKLEKLTAAENPFNCLCP 304

QY 231 LSWFGPWVRESHVTLASPEETRCHFPKNAKRLLELDVADFCGPATTTTATVPTTRPVV 290  
Db 305 LAWFPALWKDVRVELLRTETTRCHFPFINSKLEKLEHDKFCPTTTILTSGAGTSST 364  
QY 291 REPTALSSSLAPTWSLPTAPATEAPSPSTAPPTVGPVDP-----QD-----CP 335  
Db 365 SKPKNSSTQLGTYTHIVPPAP-----PSDISSADADNFPVQTTAFPPSRIMEDSSEGEIMCP 420  
QY 336 PSTCLNGGTCHLGRHHLACLCPGFTGLYCDSOMGGTRPSPT-----VTPRPPRS 388  
Db 421 PNICLNGGTCTIFKSGNVIIVCLCPPSMGNYCEIQ-NEAMLPPSPRSVLSLETIATVQNP-- 477  
QY 389 LTGLIEFVPSLRLVGLQRYLOGSSVQLRSLRTYENLSGPKELVTLRLPASLAEVTVT 448  
Db 478 -TISHHITSTLSLDLHRYIQ-TRPHIGIRLTYSNLSPDRRRLQQLSVPPSPYETLR 535  
QY 449 QLRPNATYSVCMPLQGRVPEGEAEACGEAHT---PPAVHSHNAPVQTQAREGNLPLLIAP 505  
Db 536 GLQPNSTYSCASPLGE-PHASVSACMEARTAGIPSSSHEPSVDRTERSSSLTIPIV-- 592  
QY 506 ALAAVLLAALAAVGAAYCVRRGRAMAAAOQKQGVGAGPUELGKVKVPLEPG---PK 561  
Db 593 AVAVVMVAIIAT-VVVISRRRRPKAPVMDLHE----TSPLEMEGVKTNPENGLTHPK 646  
RESULT 10  
Q503G2\_BRARE  
ID Q503G2\_BRARE PRELIMINARY; PRT; 643 AA.  
AC Q503G2;  
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.  
DT 07-JUN-2005, sequence version 1.  
DT 07-FEB-2006, entry version 5.  
DE Slit-like 2.  
GN Names:slit2;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Singapore local strain; TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Singapore local strain; TISSUE=Embryo;  
RG NIH MGC Project;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
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CC  
EMBL; BC095341; AAH95341.1; -; mRNA.



[illegible]











QY 437 RLPASLAETVTLRPNATYSVCWPLGRCRVPEGBEA-----CGEAHTPPAVHSNHAPV 491  
 DB 451 IVPASSHHFLKHLVPGADYDLCLLALSPPAGPSDLTATRLGCAHFTLSPASPLCHALQ 510  
 QY 492 TQAREGNPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAQAQKGVQPGAGPLELG 551  
 DB 511 AHVLGGLTV-----AVGGVLAALLVFTVALLV-RGRG-----AGNGRLPLKLSH 555  
 QY 552 VKVPLEPQPKAT 563  
 DB 556 VOSQTNGGSPST 567

RESULT 14  
 LRFN4\_MOUSE  
 ID LRFN4\_MOUSE STANDARD; PRT; 636 AA.  
 AC Q8XU8; Q8X3C4;  
 DT 29-MAR-2005, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JUN-2003, sequence version 1.  
 DT 07-MAR-2006, entry version 25.  
 DE Leucine-rich repeat and fibronectin type-III domain-containing protein  
 DE 4 precursor.  
 GN Name=Lrfn4;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Batalov V., Forrest A.R., Zavolan M.,  
 RA Davis M.J., Walting L.G., Aidinis V., Allen J.E., Ambesi-Impombato A.,  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
 RA Guscinich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwano A., Ishikawa T.,  
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
 RA Kitano H., Kollias G., Krishnam S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
 RA Petrovsky N., Piazza S., Reid J., Reid J.F., Ring B.Z., Ringwald M.,  
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
 RA Schonbach C., Sekiguchi K., Sempé C.A., Seno S., Sessa L., Sheng Y.,  
 RA Shibata Y., Shimada E., Shimada K., Silva D., Sinclair B.,  
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takemura Y., Taki K.,  
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 RN [2]  
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RC STRAIN=FVB/N; TISSUE=Eye, and Mammary tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
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 CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane  
 CC protein (Potential).  
 CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.  
 CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.  
 CC -!- SIMILARITY: Contains 7 LRR (leucine-rich) repeats.  
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 CC -----  
 CC EMBL; AK081560; BAC38259.1; -; mRNA.  
 DR EMBL; BC023036; AAH23036.1; -; mRNA.  
 DR EMBL; BC023156; AAH23156.1; -; mRNA.  
 DR HSSP; OSB2R6; 1P8T.  
 DR Ensembl; ENSMUSG00000045045; Mus musculus.  
 DR MGI; MGI:2385612; Lrfn4.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR013098; I-set.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR016111; LRR.  
 DR InterPro; IPR000483; LRR\_C.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR Pfam; PF00041; fn3; 1.  
 DR Pfam; PF07679; I-set; 1.  
 DR Pfam; PF00560; LRR\_1; 6.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00408; IGc2; 1.  
 DR SMART; SM00369; LRR\_TYP; 2.  
 DR SMART; SM00082; LRRCT; 1.  
 DR PROSITE; PS50853; FN3; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Glycoprotein; Immunoglobulin domain; Leucine-rich repeat; Membrane;  
 KW Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 16  
 FT CHAIN 17 636  
 FT Leucine-rich repeat and fibronectin type-  
 FT III domain-containing protein 4.  
 FT /FTID=PRO\_0000014844.  
 FT Extracellular (Potential).  
 FT Potential.  
 FT Cytoplasmic (Potential).  
 FT LRR 1.  
 FT LRR 2.  
 FT LRR 3.  
 FT LRR 4.  
 FT LRR 5.  
 FT LRR 6.  
 FT LRR 7.  
 FT Ig-like.  
 FT Fibronectin type-III.  
 FT DOMAIN 407











